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TITLE	Molecular cloning and characterization of a murine pre-B-cell growth-stimulating factor/stromal cell-derived factor 1 receptor, a murine homolog of the human immunodeficiency virus 1 entry coreceptor fusin
JOURNAL	PROC. Natl. Acad. Sci. U.S.A.
MEDLINE	97121456
REFERENCE	2 (bases 1 to 1877)
AUTHORS	Nagasawa, T.T.
TITLE	Molecular cloning of murine PBSF/SDF-1 receptor
JOURNAL	Unpublished
REFERENCE	3 (bases 1 to 1877)
AUTHORS	Nagasawa, T.
TITLE	Direct Submission
JOURNAL	Submitted (05-SEP-1996) Takashi Nagasawa, Research Institute, Osaka Medical Center, Department of Immunology, Murdoccho 840, Izumi, Osaka 590-02, Japan (E-mail: tmmunolo@sk.murcwetnet.or.jp, Tel:0725-56-11220, Fax:0725-57-3021)
FEATURES	Location/Qualifiers

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CDS
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Query Match	100.0%	Score 1877;	DB 10;	Length 1877;
Best Local Similarity	100.0%	Pred. NO. 0;		
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[illegible]

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QY	1741	GTTTGTTTTTTCAGTTTTCAAGAGTACATGTACCTCAGTCCCTCAATATGACAGTCTG	1800
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DEFINITION	1817 bp mRNA linear ROD 07-AUG-2002
IMAGE	Mus musculus, chemokine (C-X-C) receptor 4, clone MGC:36266
ACCESSION	BC031665
VERSION	BC031665.1 GI:21618781
KEYWORDS	MGC.
SOURCE	house mouse.
ORGANISM	Mus musculus

REFERENCE
AUTHORS
TITLE
JOURNAL

TITLE Direct Submission
JOURNAL Submitted (06-JUN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK
COMMENT

Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk

FOUNDER	COMMENT
<p> nan.mcc@project.umd.edu, helpc@mgc.mcl.nih.gov Contact: MGC help desk Email: cgapbs-remail.nih.gov Tissue Procurement: Gilbert Smith, Ph.D. cDNA Library Preparation: Life Technologies, Inc. </p>	

Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNI)
DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center

DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center
Center code: BCM-HGSC
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>

Center code: BCM-HSC
Web site: <http://www.hpsc.bcm.tmc.edu/cdna/>
Contact: amg@bcm.tmc.edu
Gunnarste, P.H., Garcia, A.M., Lu, X., Huljk, S.W., Hale, S.M., Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.,

Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M., Yoon, V.S., Kovacs, C.R., Lawrence, S., Martin, R.G., Muzny, D.M., Richards, S., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAK Plate: 61 Row: d Column: 24

through the I.M.A.G.E. Consortium/INLNL at: <http://image.inl.gov>
Series: IRAK Plate: 61 Row: d Column: 24
This clone was selected for full length sequencing because it
passed the following selection criteria: Similarity but not
identity to protein.

FEATURES	Location/Qualifiers
source	1. .1817

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Query Match	95.8%	Score 1797.4;	DB 10;	Length 1817;
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Db 68 GAGTGTGCCATGGAACCGATCAGTGTGAGTATATACACTCTGTGATAACTACTCTGAGA 127

QY 170 AGTGGGCTCGAGACTATGATCCACAGAACCCTGCTTCGGGATGAACGTCCA 229
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290 CAATGATTTGGTGCATCTGTGTCATGGGTTACCAAGAAAGCTAAGCAGCATGACGACAA 349

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QY	1189	ACTCCAGTAAACCTTATGCAAAAGACTTATATA---ATATATATATATATGATTAAG	1248
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DEFINITION	M.musculus mRNA for leukocyte-derived seven transmembrane domain receptor.		ROD 11-NOV-1996
ACCESSION	X99582		
VERSION	X99582.1	GI:1666648	
KEYWORDS	lestr gene; leukocyte-derived seven transmembrane domain receptor.		
SOURCE	Mus musculus.		
ORGANISM	Mus musculus.		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
AUTHORS	Moepps, B., Frodl, R., Kessler, H. and Gierschik, P.		
TITLE	cDNA cloning and genomic organization of a leukocyte-derived seven transmembrane domain receptor (LESTR) from mouse: a murine homologue of the human HIV-1 entry cofactor fusin		
JOURNAL	unpublished		
REFERENCE	2 (bases 1 to 1575)		
AUTHORS	Moepps, B.		
TITLE	Direct Submission		
JOURNAL	Submitted (19-JUL-1996) B. Moepps, Universitaet Ulm, Pharmacology/Toxicology, Albert-Einstein Allee 11, D-89081 Ulm, FRG		
REMARK	Revised by author 11-NOV-96		
COMMENT	On Nov 12, 1996 this sequence version replaced gi:1657351.		
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homologue of the human HIV-1 entry cofactor fusin

JOURNAL Unpublished
REFERENCE 2 (bases 1 to 3770)
AUTHORS Moepps, B.
TITLE Direct Submission
JOURNAL Submitted (19-JUL-1996) B. Moepps, Universitaet Ulm,
Pharmacology/Toxicology, Albert-Einstein Allee 11, D-89081 Ulm, FRG
REMARK 3 (bases 1 to 3770)
AUTHORS Moepps, B.
TITLE Direct Submission
JOURNAL Submitted (02-APR-1997) B. Moepps, Universitaet Ulm,
Pharmacology/Toxicology, Albert-Einstein Allee 11, D-89081 Ulm, FRG
COMMENT On Apr 3, 1997 this sequence version replaced gi:166646.
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BASE COUNT 824 a 934 c 947 g 1065 t
ORIGIN

Query Match 73.8%; Score 1384.6; DB 10; Length 3770;
Best Local Similarity 97.5%; Pred. No. 1.1e-276;
Matches 1442; Conservative 0; Mismatches 24; Indels 13; Gaps 3;

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QY 181 GAGACTATGACTCCACCAAGAACCGCTGCTCCGGGATGAAACGTCATTCAATAGGA 240
DB 2346 GAGACTATGACTCCACCAAGAACCGCTGCTCCGGGATGAAACGTCATTCAATAGGA 2405
QY 241 TCTTCTGCGCACCATCTACTTCATCTCTTCTTGAATGCGCATAGTCGGCAATGATGG 300
DB 2406 TCTTCTGCGCACCATCTACTTCATCTCTTCTTGAATGCGCATAGTCGGCAATGATGG 2465
QY 301 TGAATCTGTCATGGGTACACCAAGAGTAGAGCATGACGACAGTACCGGCTGC 360
DB 2466 TGAATCTGTCATGGGTACACCAAGAGTAGAGCATGACGACAGTACCGGCTGC 2525

QY 361 ACCTGTACAGTGGGTGACCTCTCTTGTGATCAGACACTCCCTTCTGGGAGTTGATGCA 420
DB 2526 ACCTGTACAGTGGGTGACCTCTCTTGTGATCAGACACTCCCTTCTGGGAGTTGATGCA 2585
QY 421 TGGCTGACTGTACTTTGGGAAATTTTGTGTAAGGCTGTCCATATCATCTACAGTGA 480
DB 2586 TGGCTGACTGTACTTTGGGAAATTTTGTGTAAGGCTGTCCATATCATCTACAGTGA 2645
QY 481 ACCTGTACAGTGGGTGACCTCTCTTGTGATCAGACACTCCCTTCTGGGAGTTGATGCA 540
DB 2646 ACCTGTACAGTGGGTGACCTCTCTTGTGATCAGACACTCCCTTCTGGGAGTTGATGCA 2705
QY 541 TCCAGCGCCACCAAGCTGCAAGGCGCAAGGAACTGTGGCTGTAAGAGGAGTATGATGG 600
DB 2706 TCCAGCGCCACCAAGCTGCAAGGCGCAAGGAACTGTGGCTGTAAGAGGAGTATGATGG 2765
QY 601 GCGTCTGATCCAGCCCTCTCTCTGATCATATACCTGATCTTCTTGGCGAGTACGCC 660
DB 2766 GCGTCTGATCCAGCCCTCTCTCTGATCATATACCTGATCTTCTTGGCGAGTACGCC 2825
QY 661 AGGGGACATCACTGACGGGGATGACAGTACATCTGTACCGCTTTACCCGATAGCC 720
DB 2826 AGGGGACATCACTGACGGGGATGACAGTACATCTGTACCGCTTTACCCGATAGCC 2885
QY 721 TGTGATGGTGGTGTTCATATCCAGCATATATATGTTGGTGTCTCATCGCCGATGCG 780
DB 2886 TGTGATGGTGGTGTTCATATCCAGCATATATATGTTGGTGTCTCATCGCCGATGCG 2945
QY 781 TCATCTCTCTCTGTACTGATCATATCATCTGATGATGATGATGATGATGATGATGATG 840
DB 2946 TCATCTCTCTCTGTACTGATCATATCATCTGATGATGATGATGATGATGATGATGATG 3005
QY 841 AGGCGAAGCCCTCAAGAGACAGTATCTCTATCTAGTTTCTTGGCTGCTGCTGCG 900
DB 3006 AGGCGAAGCCCTCAAGAGACAGTATCTCTATCTAGTTTCTTGGCTGCTGCTGCG 3065
QY 901 CATATATGAGGGGATCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 960
DB 3066 CATATATGAGGGGATCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3125
QY 961 GTGACTTCGAGACATTTGTGCAAGATGATGATGATGATGATGATGATGATGATGATGATGATG 1020
DB 3126 GTGACTTCGAGACATTTGTGCAAGATGATGATGATGATGATGATGATGATGATGATGATGATG 3185
QY 1021 ACTGTTCCTGAAACCCATCTCTATGCTTCTCTGGGGCAAAGTTCAAAAGCTCTGCC 1080
DB 3186 ACTGTTCCTGAAACCCATCTCTATGCTTCTCTGGGGCAAAGTTCAAAAGCTCTGCC 3245
QY 1081 AGCATGACATCAATCTCATGAGAGAGGCGCCAGGCTCAAGATCCTTCCAAAGAAAGC 1140
DB 3246 AGCATGACATCAATCTCATGAGAGAGGCGCCAGGCTCAAGATCCTTCCAAAGAAAGC 3305
QY 1141 GGGGTGACACTTCTCTCTGACGAGTCAAGATCTCTCAAGTTTCACTCAGCTAAC 1200
DB 3306 GGGGTGACACTTCTCTCTGACGAGTCAAGATCTCTCAAGTTTCACTCAGCTAAC 3365
QY 1201 CCTTATGCAAAAGCTTATATA----ATATATATATATATATATATATATATATATATATAT 1256
DB 3366 ACTTATGCAAAAGCTTATATA----ATATATATATATATATATATATATATATATATATAT 3425
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DB 3426 TTACATATTTCCAGATATATAGAGTGAAGTCTGATGACG----TTTTTTTTTTTT 3485
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QY 1373 TAAATA-----TGTGTTTTTGTGTTTGTGATGAGTGTGAGGAGTGTGAGGAGTGTG 1427
DB 3546 TAAATACCTTTTGTGTTTGTGTTTGTGATGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGTGTG 3605

OY 1428 CCAAGTTCTTAGTACCTTTATCTGTGTAGAGACTGTAGAAGTGTAGAGAGAACT 1487
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Db 3606 CCAAGTTCTTAGTACCTTTATCTGTGTAGAGACTGTAGAAGTGTAGAGAGAACT 3665
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OY 1488 GAACATTCAGAGTGTGTGTAATTAAGTAAGTACCGGTGATCTTGTGCTG 1547
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Db 3666 GAACATTCAGAGTGTGTGTAATTAAGTAAGTACCGGTGATCTTGTGCTG 3725
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OY 1548 CATATCTCTTCATTCGAGGAGACCCACCCGCCGCC 1586
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Db 3726 CATATCTCTTCATTCGAGGAGACCCACCCGCCGCC 3764
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RESULT 6
LOCUS MMU59760 1223 bp mRNA linear ROD 09-SEP-1996
DEFINITION Mus musculus fusin homolog mRNA, complete cds.
ACCESSION U59760
VERSION 059760.1 GI:1527134
KEYWORDS
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS Heesen, M., Berman, M.A., Gerard, C. and Dorfl, M.E.
TITLE Cloning of the mouse homologue of the human HIV co-factor gene,
fusin
JOURNAL unpublished
REFERENCE 2 (bases 1 to 1223)
AUTHORS Heesen, M., Berman, M.A., Gerard, C. and Dorfl, M.E.
TITLE Direct Submission
JOURNAL Submitted (02-JUN-1996) Pathology, Harvard Medical School, 200
Longwood Avenue, Boston, MA 02115, USA
FEATURES
source location/Qualifiers
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chemokine-receptor like"
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BASE COUNT 285 a 342 c 268 g 328 t
ORIGIN
Query Match 64.8%; Score 1216.6; DB 10; Length 1223;
Best Local Similarity 99.7%; Pred. No. 6.e-242;
Matches 1219; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY 91 ACCACACGCGCTGTAGAGGAGTGTGCATGGAACCGATCACTGTGATATATACACT 150
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Db 1 ACCACACGCGCTGTAGAGGAGTGTGCATGGAACCGATCACTGTGATATATACACT 60
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OY 151 CTGATACACTCTGGAAGAGTGGGCTCTGGAGACTATGACTCCAAAGAAAGACCTGCT 210
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Db 61 CTGATACACTCTGGAAGAGTGGGCTCTGGAGACTATGACTCCAAAGAAAGACCTGCT 120
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OY 211 TCCGGATGAAACGTCATTTCAATAGATCTTCTGCGCACCATCTCTTCATCATCT 270
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Db 121 TCCGGATGAAACGTCATTTCAATAGATCTTCTGCGCACCATCTCTTCATCATCT 180
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OY 271 TCTTGACTGGCATAGTGGCAATGATGGTGTCTGCTGATGGGTACCAAGAAAGC 330
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Db 181 TCTTGACTGGCATAGTGGCAATGATGGTGTCTGCTGATGGGTACCAAGAAAGC 240
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OY 331 TAAGAGCATGACGAGACAGTACCGGCTGACACTGTACGTGCTACTCTTTGTCA 390
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Db 241 TAAGAGCATGACGAGACAGTACCGGCTGACACTGTACGTGCTACTCTTTGTCA 300
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OY 391 TCACATCCCTTTCGGGAGTGTGATGCCATGGCTGACGTACTTTGGAAATTTTGT 450
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Db 301 TCACATCCCTTTCGGGAGTGTGATGCCATGGCTGACGTACTTTGGAAATTTTGT 360
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OY 451 GTAAGCTGTCCATATCATCTACACTGTCAACCTGTACAGACGCTTCATCTGAGCT 510
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Db 361 GTAAGCTGTCCATATCATCTACACTGTCAACCTGTACAGACGCTTCATCTGAGCT 420
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OY 511 TCATACGCTGACCGGTACTCTGCGCATTTGTCCAGCCCAACAGTCAAGGCCAAGA 570
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Db 421 TCATACGCTGACCGGTACTCTGCGCATTTGTCCAGCCCAACAGTCAAGGCCAAGA 480
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OY 571 AACTGCTGCTGAAAGGAGTCTATGTGGGCTGTGGATCCGACGCTCTCTGACTA 630
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Db 481 AACTGCTGCTGAAAGGAGTCTATGTGGGCTGTGGATCCGACGCTCTCTGACTA 540
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OY 631 TACCTGACTTCACTTTTGGCGACGTACAGCGAGGAGACATCAGTACGGGGATGACAGT 690
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OY 1231 TAT 1290
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Db 1141 TAT 1200
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OY 1291 CTTGTACAGTTTCTTTTCTTTT 1313
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Db 1201 CTTGTACAGTTTCTTTTCTTTT 1223
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RESULT 7

LOCUS	MLMCR13	1422 bp	DNA	linear	ROD 31-OCT-1996
DEFINITION	Mus musculus lcr-1 gene, exon 2.				
ACCESSION	Z80113				
VERSION	Z80113.1	GI:1655638			
KEYWORDS	CXC chemokine receptor 4; CXCR-4; lcr-1 gene.				
SOURCE	Mus musculus.				
ORGANISM	Mus musculus.				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
AUTHORS	1 (bases 1 to 1422)				
TITLE	Schubel, A., Burgstahler, R. and Lipp, M.				
JOURNAL	The mouse homologue of the human HIV coreceptor CXCR-4 (FUSIN): High expression in thymus and lymphoid tissues				
REFERENCE	Unpublished				
AUTHORS	2 (bases 1 to 1422)				
TITLE	Lipp, M.				
JOURNAL	Direct Submission				
FEATURES	Submitted (11-SEP-1996) Martin Lipp, Max-Debrueck-Center for Molecular Medicine, MDC, Robert-Rössle-Strasse 10, BERLIN-BUCH, D-13122, GERMANY				
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ORIGIN					
Query Match	61.4%; Score 1152.6; DB 10; Length 1422;				
Best Local Similarity	98.4%; Pred. NO. 1.3e-228;				
Matches 1164; Conservative	0; Mismatches 19; Indels 0; Gaps 0;				
121	TGGAACCATGAGTGTGATATACACTTGTGATTAATCTGAAAGAGGGGGTGTG	180			
11					
240	TGTCCCTGTTCCTTGTGCAGATATACACTTGTGATTAATCTGAAAGAGGGGGTGTG	299			
181	GAGACTATGACTCCACAAGAGAACCTCTCCGGGATGAAGAGCTCCATTTCATAGA	240			
300	GAGACTATGACTCCACAAGAGAACCTCTCCGGGATGAAGAGCTCCATTTCATAGA	359			
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360	TCTTCCGCCACCATCTACTTCATCATCTTCTTGACTGCGATAGTGGCGAATGGATTGG	419			
301	TGATCTTGATGGGTATACCAAGAAGAGCTAAGAGCATGACGAGCAAGTACCGCTGCG	360			
420	TGATCTTGATGGGTATACCAAGAAGAGCTAAGAGCATGACGAGCAAGTACCGCTGCG	479			
361	ACCTGTACGTGGCTACCTCTCTTGTGCATACACTCCCTTCTGGCGAGTTGATGCCA	420			
480	ACCTGTACGTGGCTACCTCTCTTGTGCATACACTCCCTTCTGGCGAGTTGATGCCA	539			
421	TGGCGATGTGAGCTTGGGAAATTTGTGTAAAGCGTGCATATCATCTACACTGTCA	480			
540	TGGCGATGTGAGCTTGGGAAATTTGTGTAAAGCGTGCATATCATCTACACTGTCA	599			
481	ACCTTACAGAGCGTTCTCATCTCTGGCGTTTCATAGCTGAGCGGTACCTCGCATTTG	540			
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QY	541	TCACAGCACCACACAGTCAAGGGCCAAAGAAAGCTGGCGTGAAGAAAGGACGTATATGG	600
Db	660	TCACAGCCACCACAGTCAAGGGCCAAAGAAAGCTGGCGTGAAGAAAGGACGTATATGG	719
QY	601	GCATCTGGATCCACAGCCCTCTCTGATATACCTGATCTTATCTTTGCCAGCTCAGCC	660
Db	720	GCATCTGGATCCACAGCCCTCTCTGATATACCTGATCTTATCTTTGCCAGCTCAGCC	779
QY	661	AGGGGAGCATGATCAGGGGGATGACAGAGTACATCTGTGACCGGCTTTACCCGATAGCC	720
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QY	721	TGTGATGATGATGTTTCAATTTCCAGCATATATAATGATGGTCTATCTGCGCGGATCG	780
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QY	781	TCATCCCTCTCTGTTACTGCATCATCTCTAAGCTGTCACTCCCAAGGGCCACACAGA	840
Db	900	TCATCCCTCTCTGTTACTGCATCATCTCTAAGCTGTCACTCCCAAGGGCCACACAGA	959
QY	841	AGCGCAAGCCCTCCAGACGACGACAGTCACTCTCATCTAGCTTTCTTGGCTGCTGGCTGC	900
Db	960	AGCGCAAGCCCTCCAGACGACGACAGTCACTCTCATCTAGCTTTCTTGGCTGCTGGCTGC	1019
QY	901	CATATATATGTGGGATCAGCATCGACCTCTTATCTTTTGGAGTCAATCAGCAAGGAT	960
Db	1020	CATATATATGTGGGATCAGCATCGACCTCTTATCTTTTGGAGTCAATCAGCAAGGAT	1079
QY	961	GTGACTTGGAGAGCATGTGTGCACAAGTGTCTCATCTACAGAGGCGCTGCCCTTCTCC	1020
Db	1080	GTGACTTGGAGAGCATGTGTGCACAAGTGTCTCATCTACAGAGGCGCTGCCCTTCTCC	1139
QY	1021	ACTGTTCCTTACACCCCATCTCTATAGCTTCTCTCGGGGCCCAAGTTCAAAAGCTCTGCC	1080
Db	1140	ACTGTTCCTTACACCCCATCTCTATAGCTTCTCTCGGGGCCCAAGTTCAAAAGCTCTGCC	1199
QY	1081	AGCATGCACTCACTCATGTAGAGAGGCTCCAGCTTCAGATCTCTTTCCAAAGAAAGC	1140
Db	1200	AGCATGCACTCACTCATGTAGAGAGGCTCCAGCTTCAGATCTCTTTCCAAAGAAAGC	1259
QY	1141	GGGGGGGACACTCTCCGCTCCACGGAGGTGAGATCTCTCAGTTTCTACCTCAGCTAAC	1200
Db	1260	GGGGGGGACACTCTCCGCTCCACGGAGGTGAGATCTCTCAGTTTCTACCTCAGCTAAC	1319
QY	1201	CCTTATGCAAGACTTAT	1260
Db	1320	CCTTATGCAAGACTTAT	1379
QY	1261	ACATTTTCCAGATATATAGAGACTGACCGAGCTTGTACAGTTT 1303	
Db	1380	ACATTTTCCAGATATATAGAGACTGACCGAGCTTGTACAGTTT 1422	
RESULT 8			
LOCUS	MMLCR12	1180 bp	mRNA
DEFINITION	Mus musculus. Icr-1 gene.		linear
ACCESSION	Z80112		
VERSION	Z80112.1		
KEYWORDS	CXC chemokine receptor 4; CXCR-4; Icr-1 gene.		
SOURCE	Mus musculus.		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
REFERENCE	Schubel, A., Burstahler, R. and Lipp, M.		
AUTHORS	The mouse homologue of the human HIV coreceptor CXCR-4 (FUSIN): High expression in thymus and lymphoid tissues		
TITLE	Unpublished		
JOURNAL	2 (bases 1 to 1180)		
REFERENCE	Lipp, M.		
AUTHORS	Direct Submission		
TITLE	Submitted (11-Sep-1996)		
JOURNAL	Martin Lipp, Max-DeBrunner-Center for		

Molecular Medicine, MDC, Robert-Roessle-Strasse 10, Berlin-BUCH,
D-13122, GERMANY
On Nov 21, 1997 this sequence version replaced gi:1542888.
FEATURES
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BASE COUNT 279 a 332 c 255 g 314 t

ORIGIN

Query Match 60.9%; Score 1143.2; DB 10; Length 1180;
Best Local Similarity 99.1%; Pred. No. 1.1e-226;
Matches 1160; Conservative 0; Mismatches 8; Indels 2; Gaps 1;

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DB 11 TCAGTATATACACTTCTGATTAATCTCTGAGAAAGTGGGGCTGGAGACTATGACTCA 70
QY 196 ACAAGAACCTCTCCGGGATGAAGAGTCCATTCATATAGATCTTCGCCCCACCA 255
DB 71 ACAGAGAACCTCTCCGGGATGAAGAGTCCATTCATATAGATCTTCGCCCCACCA 130
QY 256 TCTACTTCATCATCTTCTGACTGAGTGGCAATGGATGGTGCATCTGGTCATGG 315
DB 131 TCTACTTCATCATCTTCTGACTGAGTGGCAATGGATGGTGCATCTGGTCATGG 190
QY 316 GTTACAGAAAGTCTAGAGAGATGAGGACAAAGTACCGGGCTGCACCTGTACGTGG 375
DB 191 GTTACAGAAAGTCTAGAGAGATGAGGACAAAGTACCGGGCTGCACCTGTACGTGG 250
QY 376 ACCTCTCTTGTGCATCAGCTCCCTGTGGGCAATGGATGGTGCATCTGGTCATGG 435
DB 251 ACCTCTCTTGTGCATCAGCTCCCTGTGGGCAATGGATGGTGCATCTGGTCATGG 310
QY 436 TTGGGAAATTTTGTGAAGGCTGTCATATCATCTCAACTGTCAACTCTTACAGCAGG 495
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QY 496 TTCTCATCTGGGCTTCATCAGCTTGAGCCGGTACTCGGCATTTGCCACGCCACACA 555
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DB 491 CCCCTCTCTGACTATACCTGACTTATCTTTGGCAGCTGACGAGGGGACATCAGTC 550
QY 676 AGGGGATGACAGATACATCTGTGACCCGCTTTACCCGGATAGCTGTGATGTGTGT 735
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QY 736 TTCAATTCAGCATATATATGATGGGCTTCATCTGCGGCAATGCTCTCTCTGT 795
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DB 911 CCATCTCTATGCTCTTCTCGGGGGCCCAAGTTAAAGCTCTGCCACGATGACTCACT 970
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QY 1216 TAT 1273
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QY 1274 ATAAGAGTACAGCACTCTTGTACAGTTT 1303
DB 1151 ATAAGAGTACAGCACTCTTGTACAGTTT 1180

RESULT 9
MM065580 3366 bp DNA linear ROD 13-DEC-1996
LOCUS Mus musculus fusin (CXCR-4) gene, complete cds.
DEFINITION U65580
ACCESSION U65580.1 GI:1731650
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS Heesen, M., Berman, M.A., Benson, J.D., Gerard, C. and Dorf, M.E.
1 (bases 1 to 3366)
TITLE Cloning of the mouse fusin gene, homologue to a human HIV-1
co-factor
JOURNAL J. Immunol. 157 (12), 5455-5460 (1996)
MEDLINE 97113334
PUBMED 8955194
REFERENCE
AUTHORS Heesen, M., Berman, M.A., Gerard, C. and Dorf, M.E.
TITLE Direct Submission
JOURNAL Submitted (30-JUL-1996) Pathology, Harvard Medical School, 200
Longwood Avenue, Boston, MA 02115, USA
FEATURES
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Matches 1064; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
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LOCUS Sequence 3 from patent US 5776457.
DEFINITION
ACCESSION AR015970
VERSION AR015970.1 GI:3972247
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1. (bases 1 to 1737)
AUTHORS Lee,J. and Wood,W.I.
TITLE Antibodies to human PF4A receptor and compositions thereof
JOURNAL Patent: US 5776457-A 3 07-JUL-1998;
FEATURES
source 1..1737
BASE COUNT 454 a 411 c 373 g 499 t
ORIGIN
Query Match
Best local similarity 76.1%; Score 974.4; DB 6; Length 1737;
Matches 1391; Conservative 0; Mismatches 301; Indels 136; Gaps 10;
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DEFINITION Sequence 3 from patent US 5840856.
ACCESSION AR060748
VERSION AR060748.1 GI:5987198
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 1737)
AUTHORS Chundharapal, A., Lee, J., Hebert, C., and Kim, K. Jin.
TITLE Antibodies to a human PF4 superfamily receptor
JOURNAL Patent: US 5840856-A 3 24-NOV-1998;
FEATURES
source location/Qualifiers
1..1737
BASE COUNT 454 a. 411 c 373 g 499 t
ORIGIN

Query Match 51.9%; Score 974.4; DB 6; Length 1737;
Best Local Similarity 76.1%; Pred. No. 1.2e-191;
Matches 191; Conservative 0; Mismatches 301; Indels 136; Gaps 10;

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ACCESSION AR070433
VERSION AR070433.1 GI:7221321
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1737)
AUTHORS Lee,J. and Wood,W.I.
TITLE Nucleic acid encoding PR4A receptor
JOURNAL Patent: US 5892017-A 3 06-APR-1999;
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Best Local Similarity 76.1% Pred. No. 1.2e-191;
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RESULT 13
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LOCUS AR103430 1737 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 3 from patent US 6087475.
ACCESSION AR103430
VERSION AR103430.1 GI:12815018
KEYWORDS
SOURCE unknown.
ORGANISM unknown.
REFERENCE 1 (bases 1 to 1737)
AUTHORS Lee, J. and Wood, W. I.
TITLE PFAA receptor
JOURNAL Patent: US 6087475-A 3 11-JUL-2000;
FEATURES
source location/Qualifiers
BASE COUNT 454 a 411 c 373 g 499 t
ORIGIN
Query Match 51.9%; Score 974.4; DB 6; Length 1737;
Best Local Similarity 76.1%; Pred. No. 1.2e-191;
Matches 191; Conservative 0; Mismatches 301; Indels 136; Gaps 10;

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Dd		255	CAATGGAATTGGTCATCCGTGATGSGTTACAGAGAAGAACTGAGAAACATAGCGAGCA	314
OY		350	GTACCGGTGACCCGTGAGTGGGCTGACCTCTCTTGTCAATCACAGCCCCCTCTGGGC	409
Dd		315	GTACAGGCTGACCTGTAGTGGCCAGCCTCTCTTGTCAATCACAGCTTCCTCTGGGC	374
OY		410	AGTTGATGCCATGGCTGACTGTAATTTGGGAAATTTTGTGTAAGGCTGTCCATATAT	469
Dd		375	AGTTGATGCCGCGGGCAAACTGGTACTTTGGGAAGTCTGTATGCAAGGACGTCCATGTAT	434
OY		470	CTACACTGTCAACTCTACAGACGGCTTCTATCTCTGGCTTTCATCAGCTTGACCGSTA	529
Dd		435	CTACACATCAACCTCTACAGAGTGTCTATCTCTGGCTTTCATCAGCTTGACCGSTA	494
OY		530	CCTGCCATTTGTCACGGCCACCAACAGTCAAGGCAAGGCAAGCAAGCGCGGTGAAGAGC	589
Dd		495	CCTGGCCATTCGTCCACGGCCACCAACAGTCAAGGCAAGGCAAGCAAGCGGTGAAGAGT	554
OY		550	AGTCTATGTGGGCTCTGTGATCCACGCCCTCTCTGTGACTATACCTGACTTATCTTTGC	649
Dd		555	GGTCAATTTTGGCGTGTGATCCCGCCCTCTGTGACTATTTCCGCACTTCATCTTTGC	614
OY		650	CGAGTTCAGCAGGGGGACATCAGTCAAGGGGATATACAGGATACATCTGTGACCGCTTA	709
Dd		615	CACG-----TCAGTAGGACAGATGACAGATATATCTGTGACCGCTTGA	659
OY		710	CCCCGATAGCCTGTGATGTGTGTGTTTCAATTCACGATATATATGATGGGTCTCATCT	769
Dd		660	CCCCATATACCTTGTGGTGTGTGTGTTTCAAGTTTCAGACATCATAGTGTGGCTTATCT	719
OY		770	GCCGGGCAATGCAATCCCTCTCTGTACTGATATCATATCTCTAAGCTGTACACTCCAA	829
Dd		720	GCTTGATATGTGATCTCTCTCTGTACTGATATCATATCTCTAAGCTGTACACTCCAA	779
OY		830	GGGGCCACCAAGGCGCAAGGCCCTCAAGACAGACAGTCACTCTCATCTAGTTCCTTTGC	889
Dd		780	GGGGCCACCAAGGCGCAAGGCCCTCAAGACAGACAGTCACTCTCATCTAGTTCCTTTGC	839
OY		890	CTGCTGGCTGCATATTTATGTGGGATAGCATGCATCTTTCATCTTTTGGAGTCAT	949
Dd		840	CTGTTGGCTGCCTTACTCATTTGGGATAGCATGCATCTTTCATCTTTTGGAGTAATCT	899
OY		950	CAGCAAGAGATGTGACTCGAGAGATGTGACAGAGGATGAGATTCATCAGCAGAGGCCCT	1009
Dd		900	CAGCAAGAGATGTGACTCGAGAGATGTGACAGAGGATGAGATTCATCAGCAGAGGCCCT	959
OY		1010	GCGCTTCTTCCACTGTTGCTGTAACCCCATCTATGCTCTCTCGGGGCCAAGTTCAA	1069
Dd		960	AGCTTTCTTCCACTGTTGCTGTAACCCCATCTATGCTCTCTCTGGAGCAATTTAA	1019
OY		1070	AAGCTCTGCCAGCATGCACTCAATCOTCATGAGAGGATGACCGCCCAAGATCTTTC	1129
Dd		1020	AAGCTCTGCCAGCATGCACTCAATCOTCATGAGAGGATGACCGCCCAAGATCTTTC	1079

QY	1130	CAAGGAAAGGCGGTGACACTCTCCCTCCACGAGACAAATCCCTCACTTTTCA	1189
Db	1080	CAAGGAAAGCGAGGTGACACTTATCTGTTCCACGTAGCTCAGTCTTCAACTTTTCA	1139
QY	1190	CTCCAGCTAACCCCTTATGCAAGACCTTATATATATATATATATATGATGAAGAACTT	1249
Db	1140	CTCCAGCTTAA-----CACAGATGTATAAAGACTTTTTTTTATATAGATAAATCACTTTT	1191
QY	1250	TTTATATGTTACACATTTTCCAGATATATAGACACTGACAGCTCTGTACAGTTTTTTTTT	1309
Db	1192	TTTTATAGTTTACACATTTTTCAGATATATAAACACGACCAATATGTACAGTTTATATGC	1251
QY	1310	TTTTTAATGACGTGTGGAGATTATGTCTCCAGTATTTTGTGAGGTTTGTACTTAATTT	1369
Db	1252	TTGTTGGATTTTGTG-----CTGTGTTCTTTTAGTTTTTTGTGTAAGTTTATTTGACTTA	1305
QY	1370	ATATATATATATGTTTTTTGTTTGTTCATGTGAATGAGCGCTAGGACAGCACTGTGGCC	1429
Db	1306	TTTATATA-----TAAATTTTTTTTGTTCATTTATGATGTGTCTAGGACAGCACTGTGGCC	1361
QY	1430	AAGTCTTATAGACGTGTTTATCTGTGTGTAGGACTGTAGACTGTAGAGAAAGAACTGA	1489
Db	1362	AAGTCTTATAGACGTGTATGTCTGTGTGTAGGACTGTAGAA-----AAGGGAACATGA	1413
QY	1490	ACATTCCAGATGTGTGTGTAATTTGAATTAAGTATAGCCTAGCCGTGACTGTTGCTGCA	1549
Db	1414	ACATTCCAGACGCTGTATGTATGATACGTAAGACTAGAAATGTATCCACAGCTGTTATGCA	1473
QY	1550	TAAATCTCTTCAATCCGAGAGACACCCACCCACCCACCCACCCACCCCACTTCTTAAT	1609
Db	1474	TAGATATATCTCTCCA-----	1488
QY	1610	TGTTTGGTTATGCTGTGTGTGATGCTTTTGTTCGTTTTTTTGTGTTGTTGTTGTTT	1669
Db	1489	-----TTCCCGTGAACGTTTTCCTGTTCTTAAAGACGTAT	1525
QY	1670	TTTTCTGTAAAGATGCGACCTTAAACCAAGCCTGGAATGTGGTGAATGCTGGGGT	1729
Db	1526	TTTGTCTGTAGAGATGAGCACTTATATACCAAGCCCAAGTGTG--ATAGAAATGCTGG---	1561
QY	1730	TTTTTTGTTGTTGTTTGTTCAGATTTTCAGAGTATGATGACTTCAGTCCCTACAAT	1789
Db	1582	-----TTTTTCAGTTTTTCAGGATGGGTGATTTTCAGCCACTAC--AGT	1623
QY	1790	GTACAGCTGTATATTACATGTTTATATAAATCATGATATAACTTAATAAAAAAAAAAAAA	1849
Db	1624	GTACAGCTGTATATTACGTTGTATATAAATCATGATGTTAACTTAATAAAAAAAAAAAAA	1683
QY	1850	AAAAAAAAAAAAAAAAAAAAAAAAAAAAA	1877
Db	1684	AAAAAAAAAAAAAAAAAAAAAAAAAAAAA	1711
RESULT 14			
LOCUS	113753	113753	1737 bp DNA
DEFINITION	Sequence 4 from patent US 5440021.		Linear
ACCESSION	113753		
VERSION	113753.1	GI:996819	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 1737)		
AUTHORS	Chuntharapai,A., Hebert,C., Kim,K.J. and Lee,J.		
TITLE	Antibodies to human IL-8 type B receptor		
JOURNAL	Patent: US 5440021-A 4 08-AUG-1995;		
FEATURES	Location/Qualifiers		
SOURCE	1..1737		
BASE COUNT	454 a	411 c	373 g
ORIGIN			499 t

Query Match	51.9%	Score 974.4	DB 6:	Length 1737	
Best Local Similarity	76.1%	Pred. No. 1.2e-191			
Matches 1391:	Conservative	0	Mismatches 301	Indels 136	Gaps 10
QY	50	GCAGGTACAGTACAGCCCTCTGTAGGGGGTGTGGCTCCCGGTAAACCCACCGCTGTAGAGC	109		
DB	20	GGCGGGCGCAAGTACGCCGAGGGCCGTGATGCTCCAGTAGCCACCGCATCTGGAGAAC	79		
QY	110	GAGTGTGCCATGCAACCGATCAGTGTGATATATATACATCTTGTATTACTACTCTGAAGA	169		
DB	80	CAGCGGTATACCATGGA-----GGGGATCAGTATATATACCTTCAGTAACTACACGAGGA	134		
QY	170	AGTGGGGTCTGAGACATTAAGTACTCCAAAGAAGAACCCGTCTCCGGATGAGAAAGCTCCA	229		
DB	135	AATGGGCTACGAGGGGACTATGACTCCATCAAGAAACCCGTGTTCCTGTGAAGAAATGCTAA	194		
QY	230	TTTCAATAGATCTCTCTGCCACCATCTACTATCTCATCTCTTGTGATGGCATGTGTGG	289		
DB	195	TTTCAATAAATCTTCTCTGCCACCATCTACTCCATCATCTTCTTAATGTGGATGTGTGG	254		
QY	290	CAATGATTTGGTATCTGTGTATGGTTTACCAGAAGAAGCTTAAGAGCATAGCGACAA	349		
DB	255	CAATGATTTGGTATCTGTGTATGGTTTACCAGAAGAAGCTTAAGAGCATAGCGACAA	314		
QY	330	GTACCGGGTGACCCGTGTAGTGGCGTACCTCTCTTGTCAATCAACCTCCCTCTGTGGC	409		
DB	315	GTACGGCTGTGACCCGTGTAGTGGCGTACCTCTCTTGTCAATCAACCTCTCTGTGGC	374		
QY	410	AGTTGATCCATGCGCTGTACTGTGTAGTGGGAAATTTTGTGTAGAGCTGTCCATCAT	469		
DB	375	AGTTGATCCCGTGGCAACTGTGTACTTTGGGAAGTCTTATGCAAGGAGTCCATGTAT	434		
QY	470	CTACACTTCAACCTCTACAGACCGTTCTATCTGTGGCTTTCATCAGCCTGTGACCGGTA	529		
DB	435	CTACACACTCAACCTCTACAGAGTGTCTCATCTGTGGCTTTCATCAGCCTGTGACCGCTA	494		
QY	530	CTCGGCCATTTGGTCCAGGCCACCAACAGTCAAGGAAGGCAAGAAACGTGGCTGAAABAGC	589		
DB	485	CTCGGCCATTTGGTCCAGGCCACCAACAGTCAAGGAAGGCAAGAAACGTGGCTGAAABAGT	554		
QY	590	AGTCATATTTGGGCGTCTGTGATCCAGCCCTCTCTGTACTATATCTGATGACTTCATTTTGC	649		
DB	555	GGCTATATTTGGGCGTCTGTGATCCAGCCCTCTCTGTACTATATCTGATGACTTCATTTTGC	614		
QY	650	CGAGTCAAGCAGGGGACATCAGTCAAGGGGATGACAGGTATCTGTGACCGGCTTTTA	709		
DB	615	CAACG-----TCAGTGAAGGACAGATGACAGATATATCTGTGACCGGCTTTTA	659		
QY	710	CCCCGATAGCTGTGATGTGTGTCTTTCATTTCCAGCATTAATGTGTGGTCTATCTCT	769		
DB	660	CCCCCATATATCTGT	719		
QY	770	GCCCGGATCTGATCTCTCTGT	829		
DB	720	GCTGT	779		
QY	830	GGGCGCCAGAAAGGCGCCTTCAAGAGACAGTATCTCTCATCTAGCTTTCTTTTGC	889		
DB	780	GGGCGCCAGAAAGGCGCCTTCAAGAGACAGTATCTCTCATCTAGCTTTCTTTTGC	839		
QY	890	CTGTCTGGT	949		
DB	840	CTGT	899		
QY	950	CAGCAAGAGATGTGATCGAGAGCATTTGTGCAGCAAGAGATGTGATCGAGAGAGCCCT	1009		
DB	900	CAGCAAGAGATGTGATCGAGAGCATTTGTGCAGCAAGAGATTTTCTTACCGAGAGCCCT	959		
QY	1010	CGCCTTTTTCACATTTGTGCTGAAACCCCATCTATGCTCTTCTCGGGGCAAGTTTCA	1069		
DB	960	AGCTTTTTCACATTTGTGCTGAAACCCCATCTATGCTCTTCTTGGAGCAATTTAA	1019		
QY	1070	AAGCTTGTCCAGCATCTCAACCTCATGAGAGAGGCTTCCAGGCTTCAAGATCTTTTC	1129		

[illegible]

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BASE COUNT      454 a      411 c      373 g      499 t
ORIGIN
*
Query Match      51.9%; Score 974.4; DB 6; Length 1737;
Best Local Similarity 76.1%; Pred. No. 1.2e-191;
Matches 1391; Conservative 0; Mismatches 301; Indels 136; Gaps 10;

QY 50 GCAGGTAGAGTGCAGTCTGTGAGCGGTTGTGTGCTCCGGTAAACACACCGGCTGAGAC 109
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 20 GCGCGCGCGCAAGTGCAGCGCGGAGCGGCTAGTGTCTCCAGTACCGCATCTGGAGAC 79
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 110 GAGTGTTCAGTGAACCGCATGTGTGATATATACCTTCTGTATTAATCTGTAAGA 169
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 80 CAGCGGTACATGGA-----GGGATCAGTATATACCTTCAAGTAACTACACGAGGA 134
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 170 AGTGGGCTGAGAGTATGATCTCCACAGAGACCTCTCCGGGATGAAGAGCTCCA 229
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 135 AATGGGCTCAGGGGATATGACTCCATGAAAGAACCTTTCCTGGAAGAAATGCTAA 194
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 230 TTTCAATAGGATCTTCCGCCACCATCTACTCATCTTCTGACGTCGATAGTGG 289
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 195 TTTCAATAAATCTTCTCTCCACCATCTACTCATCTTCTTACTGCGATTTGGG 254
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 290 CAATGATTTGATCTGTGATGAGTTACAGAAAGCTAAGAGCATGACGAGCA 349
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 255 CAATGATTTGATCTGTGATGAGTTACAGAAAGCTAAGAGCATGACGAGCA 314
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 350 GATCGGCTGCACCTGTCACTGCTGCTCTTGTATACACTCCCTCTTGCGG 409
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 315 GATCAGGCTGCACCTGTCACTGCTGCTCTTGTATACACTCCCTCTTGCGG 374
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 410 AGTGTGCGCATGCTGTGATCTGTTGGAATTTTGTGAAGGCTGTCCATTCAT 469
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 375 AGTGTGCGCATGCTGTGATCTGTTGGAATTTTGTGAAGGCTGTCCATTCAT 434
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 470 CTACATGTCACCTCTACAGAGCTTCTCATCTGCTTCTCATCAGCTTGACCGGTA 529
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 435 CTACAGAGTCACCTCTACAGAGCTTCTCATCTGCTTCTCATCAGCTTGACCGGTA 494
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 530 CCGCGCATTTGTCAGCGCACCAACAGTCAAGAGGCAAGAAAGCTGCTGGAAGAGC 589
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 495 CCGCGCATTTGTCAGCGCACCAACAGTCAAGAGGCAAGAAAGCTGCTGGAAGAGC 554
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 590 AGTGTATGTGGGCTGTGATCCCAAGCTCTCTCTGACTATACCTGATTCATCTTTCG 649
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 555 GGTCTATGTGGGCTGTGATCCCAAGCTCTCTCTGACTATACCTGATTCATCTTTCG 614
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 650 CGACGTCAAGCAGGGGACATGATCAGGGGATGACAGGTACATCTGTGACCGCTTGA 709
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 615 CAACG-----TCAGTGAAGCAGATGACAGATATATCTGTGACCGCTTGA 659
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 710 CCGCGCATGCTGTGATGCTGTGTTTCAATTCAGCATATATATGCTGCTCATCT 769
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 660 CCGCGCATGCTGTGATGCTGTGTTTCAATTCAGCATATATATGCTGCTCATCT 719
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 770 GCGCGCATGCTGTGATGCTGTGTTTCAATTCAGCATATATATGCTGCTCATCT 829
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 720 GCGCGCATGCTGTGATGCTGTGTTTCAATTCAGCATATATATGCTGCTCATCT 779
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 830 GCGCGCATGCTGTGATGCTGTGTTTCAATTCAGCATATATATGCTGCTCATCT 889
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 780 GCGCGCATGCTGTGATGCTGTGTTTCAATTCAGCATATATATGCTGCTCATCT 839
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 890 CTGCTGCTGCTGATATATGCTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 949
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 840 CTGCTGCTGCTGATATATGCTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 899
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 950 CAAGCAAGATGCTGATGAGAGCTTGTGCAAGTGAATCTCATCAGAGGCGCT 1009
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 900 CAAGCAAGGCTGATGAGAGCTTGTGCAAGTGAATCTCATCAGAGGCGCT 959
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1010 CCGCTTCTTCACTGTGCTGCAACCCATCTTATGCTTCTGCGGCGCAAGTTCAA 1069
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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Db 960 ACCCTTCTTCCAGTGTGTGTGAGAACCCATCTTATGCTTCTTGTGAGCAAAATTTAA 1019
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QY 1070 AACCTTCTTCCAGTGTGTGTGAGAACCCATCTTATGCTTCTTGTGAGCAAAATTTAA 1129
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1020 AACCTTCTTCCAGTGTGTGTGAGAACCCATCTTATGCTTCTTGTGAGCAAAATTTAA 1079
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QY 1130 CAAGCAAGGCTGATGAGAGCTTGTGCAAGTGAATCTCATCAGAGGCGCT 1189
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1080 CAAGCAAGGCTGATGAGAGCTTGTGCAAGTGAATCTCATCAGAGGCGCT 1139
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1190 CTCCAGCTAACCTTATGCAAGACTTATATATATATATATATATATATATATAT 1249
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1140 CTCCAGCTAACCTTATGCAAGACTTATATATATATATATATATATATATATAT 1191
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1250 TTTTATGTTACATTTTCCAGATATATAGAGCTACAGCTTGTATACAGTTT 1309
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1192 TTTTATGTTACATTTTCCAGATATATAGAGCTACAGCTTGTATACAGTTT 1251
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QY 1310 TTTTATGTTACATTTTCCAGATATATAGAGCTACAGCTTGTATACAGTTT 1369
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Db 1252 TTTTATGTTACATTTTCCAGATATATAGAGCTACAGCTTGTATACAGTTT 1305
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QY 1370 ATATATATATATATATATATATATATATATATATATATATATATATATATAT 1429
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Db 1306 TTTTATATATATATATATATATATATATATATATATATATATATATATATAT 1361
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1430 AAGTCTTATGAGCTGTATATCTGTGTGAGAGCTGTAGAACTGTAGAGAAACCTGA 1489
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1362 AAGTCTTATGAGCTGTATATCTGTGTGAGAGCTGTAGAACTGTAGAGAAACCTGA 1413
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1490 ACATTCAGAAATGCTGTGTAATATGAAATGAACTGAGCTGATCTGCTGCA 1549
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Db 1414 ACATTCAGAAATGCTGTGTAATATGAAATGAACTGAGCTGATCTGCTGCA 1473
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1550 TATCTCTTCAATTCGAGAGCAACCCACCCACCCACCCACCCACCCACCTTAAAT 1609
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1474 TATCTCTTCAATTCGAGAGCAACCCACCCACCCACCCACCCACCCACCTTAAAT 1488
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1610 TGTGTGTTATGCTGTGATGCTGTGTTGTTTGTGTTGTTGTTGTTGTTT 1669
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1489 TGTGTGTTATGCTGTGATGCTGTGTTGTTTGTGTTGTTGTTGTTGTTT 1525
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1670 TTTTCTGTAAGATGCACTTAAACCAAGCTGAAATGTGTAGAAATGCTGGGT 1729
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Db 1526 TTTTCTGTAAGATGCACTTAAACCAAGCTGAAATGTGTAGAAATGCTGGGT 1581
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1730 TTTTCTGTTGTTGTTTTCAGTTTCAAGAGTGAATGATGATGATGATGATGAT 1789
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1582 TTTTCTGTTGTTGTTTTCAGTTTCAAGAGTGAATGATGATGATGATGATGAT 1623
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1790 GTACAGCTGTGTTATATGTTTAAATGAAATGAAATGAAATGAAATGAAATGAAAT 1849
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1624 GTACAGCTGTGTTATATGTTTAAATGAAATGAAATGAAATGAAATGAAATGAAAT 1683
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1850 AAAAAAAAAAAAAAAAAAAAAAAAAA 1877
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Db 1684 AAAAAAAAAAAAAAAAAAAAAAAAAA 1711
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Search completed: July 12, 2003, 15:58:37
 Job time : 3312 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 12, 2003, 14:05:23 ; Search time 1852 Seconds
(without alignments)
16414.108 Million cell updates/sec

Title: US-09-367-052-1

Perfect score: 1877

Sequence: 1 ccacccaataacgactcact.....aaaaaaaaaaaaaaaaaa 1877

Scoring table:

IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Search: 16154066 seqs, 8097743376 residues

Number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estrov:*
6: em_estrpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_ges:*
18: em_ges_hum:*
19: em_ges_inv:*
20: em_ges_pln:*
21: em_ges_vrt:*
22: em_ges_fun:*
23: em_ges_mam:*
24: em_ges_mus:*
25: em_ges_other:*
26: em_ges_pro:*
27: em_ges_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	684.8	36.5	1051	13	BM545259 AGENCOURT
2	631.4	33.6	958	12	BG174412 602334232
3	621.6	33.1	793	9	AA182270 mt83f01.r
4	621.2	33.1	639	9	AA1816049 vr14h02.r
5	610.2	32.5	753	13	BG915636 602814106
6	594	31.6	910	13	B1762229 603049139

7	590	31.4	955	12	BG173867	BG173867 602333928
8	578.4	30.8	891	13	B1824663	B1824663 603033815
9	576.8	30.7	950	14	BG174617	BG174617 AGENCOURT
10	576.2	30.7	628	10	AA227957	AA227957 up19e03.y
11	576	30.7	904	12	BF100790	BF100790 601753725
12	558	29.7	1034	14	BM920800	BM920800 AGENCOURT
13	552.8	29.5	765	13	BM387369	BM387369 UI-R-CN1
14	551.6	29.4	582	12	BG145042	BG145042 ut75a01.y
15	547.4	29.2	827	13	B1761664	B1761664 603046395
16	524.8	28.0	528	12	BG277031	BG277031 uv10e03.y
17	524.8	28.0	750	12	BG613352	BG613352 602641234
18	520.4	27.7	875	13	B1756157	B1756157 603030061
19	511.4	27.2	585	10	BE627479	BE627479 u052b07.y
20	509.6	27.1	913	13	BM051973	BM051973 603638877
21	509	27.1	886	12	BF101953	BF101953 601752819
22	495.8	26.4	746	13	B1917014	B1917014 603177688
23	492.6	26.2	905	13	B1754094	B1754094 603027651
24	484.2	25.8	782	12	BG685901	BG685901 602638730
25	481.6	25.7	728	9	AU117058	AU117058 AU117058
26	479	25.5	846	12	BF338608	BF338608 602034286
27	478.2	25.5	702	13	B1761118	B1761118 603043593
28	472.4	25.2	514	12	BG093377	BG093377 ut70g04.y
29	470.4	25.1	680	14	BQ109515	BQ109515 imeqec-7
30	468.4	25.0	742	13	B1597875	B1597875 603245357
31	464.2	24.7	952	13	B1821693	B1821693 603036539
32	463	24.7	703	13	B1765768	B1765768 603046522
33	453.2	24.1	658	13	B1835125	B1835125 603087792
34	447.8	23.9	917	12	BE872980	BE872980 601450675
35	443.2	23.6	645	9	A1884548	A1884548 w034a10.x
36	441	23.5	510	9	AA190052	AA190052 mu52b11.r
37	440.8	23.5	858	12	BF797340	BF797340 602256969
38	439.4	23.4	553	12	BG145062	BG145062 ut75b11.y
39	438.8	23.4	512	12	BF720603	BF720603 mab56e05.
40	435.8	23.2	671	12	BG025793	BG025793 602274794
41	426	22.7	437	12	BG093470	BG093470 ut71h04.y
42	423.2	22.5	748	13	B1546999	B1546999 603190220
43	418	22.3	446	9	A1131863	A1131863 uc36h08.r
44	411.8	21.9	484	9	AA120018	AA120018 mp93c11.r
45	410.6	21.9	561	12	BF591285	BF591285 7044g03.x

ALIGNMENTS

RESULT 1
LOCUS BM545259 1051 bp mRNA linear EST 20-FEB-2002
DEFINITION AGENCOURT_6497171 NIH_MGC_124 Homo sapiens CDNA clone IMAGE:5726963
ACCESSION BM545259
VERSION BM545259.1 GI:18777197
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE NIH-MGC <http://mgs.nci.nih.gov/>
1 (bases 1 to 1051)
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contract: Robert Strausberg, Ph.D.
COMMENT Email: cgapbs-remail.nih.gov
Tissue Procurement: Invitrogen
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Place: LLA012720 row: e column: 12
High quality sequence start: 20
High quality sequence stop: 753.
Location/Qualifiers

FEATURES


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QY 114 GTTGGCATGGAACCGATGAGTGTGATATATACACTTGTGATACTACTGAGAAGTG 173
Db 61 GTTGGCATGGAACCGATGAGTGTGATATATACACTTGTGATACTACTGAGAAGTG 120
QY 174 GGGTCTGGAGACTATGACTCCACAAGAACCCCTGCTCCGGGANGAAGCACTCCATTTC 233
Db 121 GGGTCTGGAGACTATGACTCCACAAGAACCCCTGCTCCGGGANGAAGCACTCCATTTC 180
QY 234 AATGAGATCTGCTGCTCCACCATCTACTCATCTCTTCTTACCTGGCATAGTCGGCAT 293
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QY 294 GGATTGGTATCTGCTGCTGATGAGTTACAGAGAAGCTAAGAGAGCATGACGACAGATGAC 353
Db 241 GGATTGGTATCTGCTGCTGATGAGTTACAGAGAAGCTAAGAGAGCATGACGACAGATGAC 300
QY 354 CGGCTGACACTGTCAAGTGGCTGACCTCTCTTTGTATCATCACTCCCTTCTGGGCAATT 413
Db 301 CGGCTGACACTGTCAAGTGGCTGACCTCTCTTTGTATCATCACTCCCTTCTGGGCAATT 360
QY 414 GATGGCATGAGCTGATGCTGACTTTGGGAATTTTGTGTAAGGCTTCCATATCATCTAC 473
Db 361 GATGGCATGAGCTGATGCTGACTTTGGGAATTTTGTGTAAGGCTTCCATATCATCTAC 419
QY 474 ACTGTCAACCTTACAGACAGCTTCTCATCTGACCTTCTCATGAGCTTGGACGGTACCTC 533
Db 420 ACTGTCAACCTTACAGACAGCTTCTCATCTGACCTTCTCATGAGCTTGGACGGTACCTC 479
QY 534 GCCATTGTCCACGACCAACAGTCAAGAGCCAGGAAACCTGTGGCTGAAAAAGGCAATC 593
Db 480 GCCATTGTGTCCACGACCAACAGTCAAGAGCCAGGAAACCTGTGGCTGAAAAAGGCAATC 539
QY 594 TATGTTGGGCTGTGATGCCAGCTCTCTCTGACTATATCCGACTTCTTCTTGGCCAGC 653
Db 540 TATGTTGGGCTGTGATGCCAGCTCTCTCTGACTATATCCGACTTCTTCTTGGCCAGC 598
QY 654 GTACAGCCAGAGGGGAGATCATGATCAGAGGGGATGACAGGTATCATCTGTACCGCTTCC 713
Db 599 GTACAGCCAGAGGGGAGATCATGATCAGAGGGGATGACAGGTATCATCTGTACCGCTTCC 658
QY 714 GATGACCTGTGATGATGCTGTGTTTCATTAATTCAGCATATATAGTGGTCTCATCTCG 770
Db 659 TA---GCTGTGATGAGGGGCG--TTCAACTCCAGCATATAGAGGGGTCATCTCGCG 711
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RESULT 3

A182270

DEFINITION

793 bp mRNA linear EST 06-JAN-1997
mt83f01.r1 Soares mouse lymph node NbMLN Mus musculus cDNA clone
IMAGE:636505.5, similar to gb:106797 PROBABLE G PROTEIN-COUPLED
RECEPTOR LCRI HOMOLOG (HUMAN), mRNA sequence.

A182270.1 GI:1765810

ACCESSION

A182270.1 GI:1765810

VERSION

A182270.1 GI:1765810

KEYWORDS

EST.

SOURCE

house mouse.

ORGANISM

Mus musculus

REFERENCE

1 (bases 1 to 793)

AUTHORS

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

TITLE

The WashU-HMI Mouse EST Project

JOURNAL

Unpublished (1996)

COMMENT

Contact: Maria M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810

Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LBNL; contact the
IMAGE Consortium (info@image.lbnl.gov) for further information.
MGI:388497
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 497.
Location/Qualifiers

FEATURES

source

1..793
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:636505"
/clone_lib="Soares mouse lymph node NbMLN"
/sex="male"
/tissue_type="lymph node"
/dev_stage="4 weeks"
/lab_host="DH10B"
/note="Organ: lymph node; Vector: pT73D-Pac (Pharmacia)
with a modified polylinker; Site 1: Not I; Site 2: Eco RI;
1st strand cDNA was primed with a Not I - oligo(dT) primer
15',
normalized by Dr. Bertrand Jordan, library constructed and
provided by Dr. Bento Soares and M. Fatima Bonaldo."
BASE COUNT 181 a 202 c 175 g 222 t 13 others
ORIGIN

Query Match

Best Local Similarity 92.4%; Pred. No. 1,1e-65;

Matches 715; Conservative 0; Mismatches 46; Indels 13; Gaps 6;

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Db 1 CCTGACTCATCTTTGCCAGCTCAGCCAGGGGGACATCATGAGGGGATGACAGCTAC 60
QY 693 ATCTGTGACCGCTTTACCCCGATAGCCCTGTGATGATGATGATGATGATGATGATGAT 752
Db 61 ATCTGTGACCGCTTTACCCCGATAGCCCTGTGATGATGATGATGATGATGATGATGAT 120
QY 753 ATGTTGGGCTCATCTGCGCGGATCATCTCTCTCTGTTAGTGCATCATCTCT 812
Db 121 ATGTTGGGCTCATCTGCGCGGATCATCTCTCTCTGTTAGTGCATCATCTCT 180
QY 813 AAGCTGTCACTTCAAGAGGCGCACGAGAGCGGAGCCCTCAGAGCAGTATCTCT 872
Db 181 AAGCTGTCACTTCAAGAGGCGCACGAGAGCGGAGCCCTCAGAGCAGTATCTCT 239
QY 873 ATCTGTGACCGCTTTACCCCGATAGCCCTGTGATGATGATGATGATGATGATGATGAT 932
Db 240 ATCTGTGACCGCTTTACCCCGATAGCCCTGTGATGATGATGATGATGATGATGATGAT 299
QY 933 ATCTGTGACCGCTTTACCCCGATAGCCCTGTGATGATGATGATGATGATGATGATGAT 992
Db 300 ATCTGTGACCGCTTTACCCCGATAGCCCTGTGATGATGATGATGATGATGATGATGAT 359
QY 993 TCCATTCACAGAGGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1052
Db 360 TCCATTCACAGAGGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 419
QY 1053 CTGCGGGCCAAATTCAAAAGCTCTGCGGATGATGATGATGATGATGATGATGATGAT 1112
Db 420 CTGCGGGCCAAATTCAAAAGCTCTGCGGATGATGATGATGATGATGATGATGATGAT 479
QY 1113 AGCTTCAGATCTTCTTCAAGAGGCGGGGATGATGATGATGATGATGATGATGATGAT 1172
Db 480 AG-CTTAAATCTCTT-CAAAGAGAGCGGGGATGATGATGATGATGATGATGATGATGAT 537
QY 1173 GAATCTCCAGTTTTCATCTCAGCTTAACCTTATGCAAGAGTATATA----ATATATA 1228
Db 538 GAATCTCCAGTTTTCATCTCAGCTTAACCTTATGCAAGAGTATATAATATATATA 597
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QY 1229 TATATATATGATAAGAACTTTTATGTTACACATTTCCAGATATAGAGACTGACCA 1288
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QY 1289 GTCTGTGACAGTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 1348
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QY 1349 TTGTGAGGTTGACATTTATTTATTTATTTTATTTTATTTTATTTTATTTTATTTT 1402
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DB 712 TTGTGAGGTTGACATTTATTTATTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 765

RESULT 4
AA816049 639 bp mRNA linear EST 13-FEB-1998
LOCUS V114h02.r1 Barstead mouse myotubes MRLB5 Mus musculus cDNA clone
DEFINITION IMAGE:1120659 5' similar to gb:L06797 PROBABLE G PROTEIN-COUPLED
RECEPTOR LCRI HOMOLOG (HUMAN); mRNA sequence.
AA816049
AA816049.1 GI:2885645
EST
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 639)
Marras, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.
The WashU-HMI Mouse EST Project
Unpublished (1996)
Contact: Maria M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:609995
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 510.
Location/Qualifiers
1..639
/organism="Mus musculus"
/strain="C3H"
/db_xref="taxon:10090"
/clone="IMAGE:1120659"
/clone_1ib="Barstead mouse myotubes MRLB5"
/cell_line="C2C12"
/lab_host="DHI08"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker. Site1: EcoRI, Site 2: NotI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5'
TGTACGATCTGAAAGTGGAGCGCCGCTTTTATTTTATTTTATTTTATTTTATTTTATTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors
[AATTCGGATCTGTG], digested with Not I and cloned into the
Not I and Eco RI sites of the modified pT73 vector.
Library constructed by Bob Barstead. The C2C12 cell line
(available from ATCC, catalog # CRL-1772) differentiates
rapidly, forming contractile myotubes and producing
characteristic muscle proteins."

BASE COUNT 149 a 178 c 126 g 186 t

Query Match 33.1%; Score 621.2; DB 9; Length 639;
Best Local Similarity 99.5%; Pred. No. 1.5e-65;
Matches 623; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 688 GGTACATCTGTGACCGCCCTTTACCCGATAGCCGTGATGGTGTGTTCAATTCCAGC 747
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DB 14 GGTACATCTGTGACCGCCCTTTACCCGATAGCCGTGATGGTGTGTTCAATTCCAGC 73
QY 748 ATATATAGTGGTGTCTATCTGCTGCGGCGATCGATCTCTCTCTGTTAGTGCATCATCA 807
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DB 74 ATATATAGTGGTGTCTATCTGCTGCGGCGATCGATCTCTCTCTGTTAGTGCATCATCA 133
QY 808 TCTCTAGCTGTCAACATCTCAAGGGCCACCGAAGCCGATCCCTCAAGAGCAGATCA 867
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DB 134 TCTCTAGCTGTCAACATCTCAAGGGCCACCGAAGCCGATCCCTCAAGAGCAGATCA 193
QY 868 TCTCTATCTGATCTTTCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 927
|||||
DB 194 TCTCTATCTGATCTTTCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 253
QY 928 CCTTCATCTCTTTTGGGAGTCAATCAAGCAAGATGTGACTTGCAGAGCATTTGTCACAGT 987
|||||
DB 254 CCTTCATCTCTTTTGGGAGTCAATCAAGCAAGATGTGACTTGCAGAGCATTTGTCACAGT 313
QY 988 GGATCTCCATCAACAGAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1047
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DB 314 GGATCTCCATCAACAGAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 373
QY 1048 CCTTCCTGGGGGCCAAGTTCAAAAGCTGCGCCAGCATGCACTCAATGCATGAGCAGAG 1107
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DB 374 CCTTCCTGGGGGCCAAGTTCAAAAGCTGCGCCAGCATGCACTCAATGCATGAGCAGAG 433
QY 1108 GCTCCAGCCCTCAAGATCTCTTTCCAAAGGAGGAGGAGTGTGACATCTTCCGTCCACGG 1167
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DB 434 GCTCCAGCCCTCAAGATCTCTTTCCAAAGGAGGAGGAGTGTGACATCTTCCGTCCACGG 493
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DB 494 AGTCAGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 553
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DB 554 ATATATATATGATTAAGAACTTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 613
QY 1288 ACTCTGTGACAGTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 1313
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DB 614 ACTCTGTGACAGTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 639

RESULT 5
BG915636 753 bp mRNA linear EST 05-JUN-2001
LOCUS 602814106F1 NCI_CGAP_Mam4 Mus musculus cDNA clone IMAGE:4936465 5',
DEFINITION mRNA sequence.
ACCESSION BG915636
VERSION BG915636.1 GI:14296112
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 753)
NIH-MGC <http://mgc.nci.nih.gov/>,
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furch
Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: LLM10868 row: 1 column: 02

FEATURES
source

High quality sequence stop: 683.
Location/Qualifiers

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/dev_stage="5 months"
/lab_host="DH10B"
/note="Organ: mammary; Vector: pCMV-Sport6; Site: 1: SalI; Site: 2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Priscilla Furth. NIH Reference for transgenic model: Li et al., Cell Growth and Differentiation 7, 5-11 (1996)."

BASE COUNT

175 a 204 c 189 g 185 t

Query Match 32.5%; Score 610.2; DB 13; Length 753;
Best Local Similarity 98.1%; Pred. No. 2.7e-64;

Matches 670; Conservative 0; Mismatches 8; Indels 5; Gaps 5;

50 GCAGGTACAGTACCTCTGTGAGGGTTGGTGTCTCCGGTACACACACGGCTGTAGAGC 109
10 GGAGGTACAGTACCTCTGTGAGGGTTGGTGTCTCCGGTACACACACGGCTGTAGAGC 69
110 GAGTGTCCCATGAGAACCGATCAGTGTATATACACTTGTGATTAATCTCTGAAGA 169
70 GAGTGTCCCATGAGAACCGATCAGTGTATATACACTTGTGATTAATCTCTGAAGA 129
170 AGTGGGCTGTGAGACTATGACTCCACAGAGAACCTCCGGGATGANAACGTCCA 229
130 AGTGGGCTGTGAGACTATGACTCCACAGAGAACCTCCGGGATGANAACGTCCA 189
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470 CTACACTGTCAACCTCTACAG-CAGCGTTTCATCTTGGCCCTTCATCAGCTTGGACCGGT 528
429 CTACACTGTCAACCTCTACAGCTGCTGCTTCATCTTGGCCCTTCATCAGCTTGGACCGGT 488
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489 ACCTGCGCATTTGTCCAGCCACCAACAGTCAAGAGCAAGAAATGCTGGTGAAG-AAG 548
588 GCAGTCTATGTGGGCTGTGATCCAGCCCTCTCTGACTATACCTGACTTTCATCTT 647
549 GCAGTCTATGTGGGCTGTGATCCAGCCCTCTCTGACTATACCTGACTTTCATCTT 608
648 GCCGAGTGTAGGAGGAGGAGATCAGTACAGG-GGATGACAGGTACATCTGTGACCGCT 706
609 GCCGAGTGTAGGAGGAGGAGATCAGTACAGG-GGATGACAGGTACATCTGTGACCGAT 668
707 TTACCCCGATAGCTGTGGATGG 729
669 TTA-CCCGATAGCTGTGTATAG 690

RESULT 6
BI762229 910 bp mRNA linear EST 25-SEP-2001
LOCUS 603049139P1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5189552 5',
DEFINITION mRNA sequence.

ACCESSION BI762229
VERSION BI762229
KEYWORDS EST.
SOURCE human.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE

NIH-MGC http://mhc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

TITLE

JOURNAL

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LAM11473 row: m column: 09

High quality sequence stop: 827.
Location/Qualifiers

FEATURES
source

1..910

/organism="Homo sapiens"
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/clone_image="5189552"
/clone_lib="NIH_MGC_116"
/lab_host="DH10B"
/note="Organ: pooled colon, kidney, stomach; Vector: pCMV-Sport6; Site: 1: NotI; Site: 2: EcoRV (destroyed); RNA source anonymous pool of 3 colons, age 26 yo male, 49 yo female, 71 yo male colon; 46 yo male kidney, and pool of 2 stomachs, 62 yo male and 70 yo female. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 023. Note: this is a NIH_MGC Library."

BASE COUNT

210 a 260 c 208 g 232 t

Query Match 31.6%; Score 594; DB 13; Length 910;
Best Local Similarity 80.8%; Pred. No. 2e-62;

Matches 750; Conservative 0; Mismatches 155; Indels 23; Gaps 4;

50 GCAGGTACAGTACCTCTGTGAGGGTTGGTGTCTCCGGTACACACACGGCTGTAGAGC 109
3 GCAGGTACAGTACCTCTGTGAGGGTTGGTGTCTCCGGTACACACACGGCTGTAGAGC 62
110 GAGTGTCCCATGAGAACCGATCAGTGTATATACACTTGTGATTAATCTCTGAAGA 169
63 CAGCGGTTACATGGA-----GGGATCAGTATATATACACTTGTGATTAATCTCTGAAGA 117
170 AGTGGGCTGTGAGACTATGACTCCACAGAGAACCTCCGGGATGANAACGTCCA 229
118 AATGGGCTGTGAGACTATGACTCCACAGAGAACCTCCGGGATGANAACGTCCA 177
230 TTTCATATAGATCTTCTGCCCCACCATCTACTTTCATCATCTTCTGACTGGCATAGTGG 289
178 TTTCATATAAATCTTCTGCCCCACCATCTACTTTCATCATCTTCTGACTGGCATAGTGG 237
290 CAATGATTTGGTATCGTGCATCGGTGTTACAGAGAAAGCTAAGGAGATACGGACAA 349
238 CAATGATTTGGTATCGTGCATCGGTGTTACAGAGAAAGCTAAGGAGATACGGACAA 297
350 GTACCGGCTGCACCTGTGAGTGGTACCTCTTTCATCATCTTCTGACTGGCATAGTGG 409

Db 298 GTACAGGCTGACCTGTGAGTGGCCGACCTCTCTTGTGACATCAGCGTTCCCTCTGGGC 357
Oy 410 AGTTATATCCATGGCTGACTGTACTTTGGGAAATTTTGTGAAGCGCTTCATATATAT 469
Db 358 AGTTATATCCGCTGAACTGTACTTTGGGAACTTCTATGCAAGGACATGTCATGTAT 417
Oy 470 CTACATCTCAACCTCTACAGAGCGTTCTCATCTCTGGCGTTTCATCAGCGTGCAGCGGTA 529
Db 418 CTACAGATCAACCTCTACAGAGAGTGTCTCTCTCTGGCGTTTCATCAGCGTGCAGCGGTA 477
Oy 530 CCTGCGCATTTGTCCAGCGCCACCAACAGTCAAGGCGGAAAGAAAGCTGTGCTGAAGAGC 589
Db 478 CTTGGCCATGCTCCAGCGCCACCAACAGTCAAGGCGGAAAGAGCTGTGCTGAAGAGT 537
Oy 590 AGTATATGTTGGCGCTGTGATGCCAGCGCTCTCTCTGATATATCTGATCTTATCTTGGC 649
Db 538 GGTCTATGTGTGGCTGTGATGCCAGCGCTCTCTCTGATATATCTGATCTTATCTTGGC 597
Oy 650 CGACGTCAGCGCGGAGCATCATGTCAGGCGGATGACAGTACATCTGTGACCGCGTTTGA 709
Db 598 CAACG-----TCAGTGAAGGAGATCAGATATATCTGTGACCGCGTTTGA 642
Oy 710 CCCCAGATACCTGTGATGTGTGTTCATTCAGATATATATGTGGGTCTGATCT 769
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Oy 889 CCTGCTGCTGCATATATATGTGGGATCAGATGACT--CCTTCATCTTTTGGAGT 946
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RESULT 7
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DEFINITION Bg173867 955 bp mRNA linear EST 06-PEB-2001
6023332861 NCI_CGAP_Mam1 Mus musculus cDNA clone IMAGE:4457119 5',
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LOCATION Bg173867
Bg173867.1 GI:12680570
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 955)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
Email: c9apbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLM10253 row: g column: 08
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/tissue_type="tumor, biopsy sample"
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/lab_host="DH10B"
/note="organ: mammary; Vector: pCMV-Sport6; Site:1; SalI;
Site:2; NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"

BASE COUNT 218 a 255 c 236 g 246 t
ORIGIN

Query Match 31.4% Score 590; DB 12; Length 955;
Best Local Similarity 90.5%; Pred. No. 5.7e-62;
Matches 724; Conservative 0; Mismatches 55; Indels 21; Gaps 8;

Oy 73 GCGTTTGGTGTCCGGTAAACCAACGAGCGTGAAGAGAGTGTGACATGAGACGATCA 132
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Oy 253 CCATCTACTTATCATCTCTTCTGACTGCGATAGTGGCAATGATGTGATCTCTGATCA 312
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Oy 487 ACAGCAGCGTGTCTATCTGCGCTTTCATCAGCTGAGACCGGTACCTGCCATTGTCACG 546
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Db 541 GGATCCAGCGCTCTCTGACTATCTGACTGATCTTGTGCGA--CGTACGACGAGGG 600
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Oy 722 ----GTGATAGTGTGTTTCAATTCACGATATTA--TGTGGGTCTATCTGCGCGGC 776
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Oy 777 A-----TGTCAATCTCTCTGATCTGATCATATCTCTGAGGTCACGATCAAGGG 832
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Db      780 CACCAGAGAAGGCGACGGCTC 799

RESULT_8
BI824663
LOCUS
DEFINITION
B1824663
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 891)
NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)
DNA Sequencing by: Inyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LMNL at:
http://image.lnl.gov
Plate: LMAM1435 row: n column: 03
High quality sequence stop: 827.

FEATURES
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Location/Qualifiers
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/lab_host="DH10B"
/note="Organ: pooled brain, lung, testis; Vector: pCMV-Sport6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; 1 male lung, age 27; and 1 male testis, age 69. Library is oligo-dt primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH/MGC library."

Query Match          30.8%; Score 578.4; DB 13; Length 891;
Best Local Similarity 80.2%; Pred. No. 1.5e-60;
Matches   725; Conservative    0; Mismatches 156; Indels   23; Gaps     3;

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                ACTCGATCAAGAACTGAGAAAGCTCATTGCCAATGAGATCTCCCTGC 249
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OY		370	TGGGTGACCTCCCTTTTGTCATCAGCACGCCCTTGTGGGAGTTGGATGCATGGCTACT	422
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Dd		419	GCAGTGTCTCTATCCTGTGCGCTTCATCATGCTGTGAGACCGGTACCTGGCCATCTCTCACGCCA	478
OY		550	CCAACAGTCAAAAGGCCAAGGAAACTGGCTGGGTGAAAAAGGAGTGTATGTGGGGCTGTGGA	609
Dd		479	CCAAAGTCAAGAAGGCCAAGGAGAGCTGTTGGCTGAAGAAGTGTCTATGTGTGGCTGTGGA	538
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Dd		645	TTTGTTTCCAGTTTTCAGACACATCATGTGTGGCCCTTATJCTGTGCTGTGATTTGTCAATCCTGT	704
OY		790	CCTGTATTCGATCATCATCTCTTAAGCTGTGCACACTCCCAAGGGCCACAGAGGCGCAAG	849
.Dd		705	CCGTGATATTCATATCATCTTCCAAAGCTGTCCAACTCCAAAGGGCCACAGAGGCGCAAG	764
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Dd		765	GCCCTCAAAGACACACAGCTCATCCCTCATCTCTGTGTTCTTTCGCCCTGTGGCTCTTACT	824
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Dd		825	ACATTGGGAATCAGCATCATCACTCTCTCATCTCTCTCGAATCATCATCAGCAAGGCTGTAG	884
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Dd		885	TTTG 888	
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DEFINITION		IMAGE:GI934537	Lupski,symathetic_trunk Homo sapiens cDNA clone	
VERSION		AGNE:6193609 5'	mRNA sequence.	
KEYWORDS		BQ718617.1	GI:21857514	
SOURCE		EST.		
ORGANISM		Homo sapiens		
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS		Mammalia; Euteria; Primates; Catarrhini; Hominiidae; Homo.		
TITLE		1 (bases 1 to 950)		
JOURNAL		NIH-MGC http://mgc.nci.nih.gov/.		
COMMENT		National Institutes of Health, Mammalian Gene Collection (MGC)		
		Unpublished (1999)		
		Contact: Robert Strausberg, Ph.D. *		
		Email: cgapbs-remail.nih.gov		
		Tissue Procurement: Dr. James R. Lupski		
		cDNA Library Preparation: Life Technologies, Inc.		
		cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)		
		DNA sequencing by: Agencourt Bioscience Corporation		
		Clone distribution: MGC clone distribution information can be		
		found through the I.M.A.G.E. Consortium/LNLN at:		
		http://image.lnl.gov		
		Plate: LLM13597 row: 1 column: 02		
		High quality sequence stop: 659.		

source

1. 765
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/strain="Sprague-Dawley"
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/clone="UI-R-CNI-cj1-9-19-0-UI"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker. Site 1: Not I; Site 2: Eco RI; The UI-R-CNI library is a subtracted library derived from the following pool of seven normalized rat libraries: normalized rat seminal vesicles, normalized rat penis, normalized rat bladder, normalized rat cervix, normalized rat brown adipose, normalized rat fundus, and normalized rat salivary gland. It was constructed according to the procedure described by Bonaldo, Lennon & Soares (genome Research genome 6: 791-806, 1996). For construction of the CNI library, plasmid DNA from the pool of normalized libraries was electroporated into competent bacteria for the production of single-stranded circular DNA. This was then used as a tracer in a subtractive hybridization with a driver (PCR amplified inserts from a plasmid DNA template preparation) comprising: a) a pool of about 34,000 clones from the Rat Unigene Set corresponding to plates R-5-AA-NN excluding plates R-5-MM and MN. This pool represented 40% of the final driver population. b) a pool of about 29,000 clones from subtracted libraries CA0 and CA1 corresponding to plates R-CA0-AMV through R-CA0-AXS, R-CA0-AXX through R-CA0-BAZ, R-CA0-BFE through R-CA0-BHY, R-CA0-BJS, R-CA0-BKE, R-CA0-BKG-H, R-CA0-BKJ-K, R-CA0-BKP through R-CA0-BKS, R-CA0-BKU-V, R-CA0-BLY through R-CA0-BMA, R-CA0-BMC through R-CA0-BME, R-CA0-BNS, R-CA0-BOB through R-CA0-BOJ, R-CA0-BPA through R-CA0-BPG, R-CA0-BBA through R-CA1-BDA, R-CA1-BHZ through R-CA1-BUF, R-CA1-BJR, R-CA1-BJT through R-CA1-BKE, R-CA1-BKD, R-CA1-BKF, R-CA1-BKI, R-CA1-BKT, R-CA1-BLE, R-CA1-BLH through R-CA1-BLN, R-CA1-BLS, R-CA1-BLU-V, R-CA1-BMN, and R-CA1-BLE. The resulting pool represented 20% of the final driver population. c) a pool of about 15,000 clones from non-normalized libraries CS0s, CT0s, CU0s, CM0s, CX0s and normalized libraries CS0, CT0, CU0, CM0, and CX0 corresponding to plates R-CS0s-CBD through R-CS0s-CBO, R-CT0s-CAM through R-CT0s-CAX, R-CU0s-CBP through R-CU0s-CCA, R-CM0s-CCB through R-CM0s-CCM, R-CX0s-CCN through R-CX0s-CCX, R-CS0-BSD, R-CS0-BTD through R-CS0-BTV, R-CS0-BVM, R-CT0-BTW through R-CT0-BUP, R-CT0-BVN, R-CU0-BUX through R-CU0-BVL, R-CM0-BVY through R-CM0-BWP, R-CX0-BXN through R-CX0-BXO, R-CX0-BWQ through R-CX0-BXM. The resulting pool represented 5% of the final driver population. d) a pool of about 5,000 clones (1,000 from non-normalized eye library CV0 and 4,000 from normalized eye library CV1) corresponding to plates R-CV0-BRH through R-CV0-BRR, R-CV1-BRS through R-CV1-BSC, R-CV1-BSE through R-CV1-BTC, and R-CV1-BVO through R-CV1-BVU. This pool represented about 5% of the final driver population. e) A pool of about 10,000 clones from subtracted library BS2, BV0 and BVOP (7-9.5 kb cDNA library fraction from rat whole embryo), and BX0 (0.5-7kb cDNA library fraction from rat whole embryo) corresponding to plates R-BS2-BDB through R-BS2-BFB, R-BV0-ANK through R-BV0-ANR, R-BVOP-AOI through R-BVOP-AOX, and R-BX0-AOY through R-BX0-ASH. The resulting pool represented 5% of the final driver population. f) a pool of about 7,000 clones from the seven non-normalized libraries that make up the tracer including CY0, CZ0, DA0, DB0, DC0, DD0, and DE0 corresponding to plates R-CY0-BXP through R-CY0-BXZ, R-CZ0-BYA through R-CZ0-BYL, R-CZ0-BZB-C, R-DA0-BXZ through R-DA0-BYP, R-DA0-BZD through R-DA0-BZH, R-DB0-BYQ through R-DB0-BZA, R-DC0-BZI through R-DC0-BZO, R-DD0-CAY through R-DD0-CBA, R-DD0-BZR through R-DD0-CAI, R-DD0-CBB-C, and R-DD0-CAB through R-DD0-CAL. The resulting pool represented about 10% of the final driver

population. g) a pool of about 2,000 clones from the pool of normalized libraries, CU0, that makes up the tracer. The corresponding plates are R-CNO-BKW through R-CNO-BLD, R-CNO-BLG, R-CNO-BLP through R-CNO-BLR, R-CNO-BLT, R-CNO-BLW-X, R-CNO-BMB, and R-CNO-BMF through R-CNO-BML. This pool represented 5% of the final driver population. h) a pool of the 28 most abundant clones in the CNO pool corresponding to the following addresses: bkx-a-09-0-UI, bkx-b-09-0-UI, bkx-b-11-0-UI, bkx-b-10-0-UI, bkx-d-01-0-UI, bkx-d-06-0-UI, bkx-g-08-0-UI, bkx-h-12-0-UI, bkx-a-05-0-UI, bkz-a-06-0-UI, bkz-a-11-0-UI, bkz-c-06-0-UI, bkz-c-09-0-UI, bkz-d-10-0-UI, bla-a-01-0-UI, bla-a-02-0-UI, bla-f-04-0-UI, bla-g-07-0-UI, bla-g-12-0-UI, bla-h-12-0-UI, blb-f-02-0-UI, blc-a-11-0-UI, blc-e-95-0-UI, bid-1-08-0-UI, bid-f-02-0-UI, bid-g-04-0-UI, blr-a-05-0-UI, blt-f-08-0-UI. This pool represented 5% of the final driver population. i) One abundant CNO clone (corresponding to the address bkz-a-11-0-UI) was digested with Not I and Eco RI and the resulting insert was gel purified. This purified insert was added directly to the driver so that it represented 5% of the final driver population.
TAG-LIB-UI-R-CNI
TAG-TISSUE-cervix
TAG-SEO-GACCA"

BASE COUNT	157 a	211 c	194 g	202 t	1 others
ORIGIN					
Query Match	29.5%	Score 552.8;	DB 13;	Length 765;	
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Matches 609;	Conservative 0;	Mismatches 52;	Indels 15;	Gaps 1;	
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105	TGGAATATACACTGCTGATACACTGCTGAGAGAGGGGTGCGAGATGATGACCA	164			
196	ACAAGGAACCCCTGCTCCGGGATGAAACGTCATTCATAGAGATCTTCCTGCCACCA	255			
165	ACAAGGAACCCCTGCTCCGGGATGAAACGTCATTCATAGAGATCTTCCTGCCACCA	224			
256	TCTACTTCATCATCTTCTTCTGAGCATAGTGGCATGATGATGATGATGATGATG	315			
225	TCTATTTATATATCTTCTGAGCATAGTGGCATGATGATGATGATGATGATGATG	284			
316	GTTACGAGAAACCTGAG	375			
285	GTTACGAGAAACCTGAG	344			
376	ACCTCTCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	435			
345	ACCTCTCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	404			
436	TTGGGAATTTTGTGAGAGCTGTCATATCATCTACACTGTACACTGTACAGCAGC	495			
405	TTGGGAATTTTGTGAGAGCTGTCATATCATCTACACTGTACACTGTACAGCAGC	464			
496	TTTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	555			
465	TTTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	524			
556	GTCGAAGCCAGGAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	615			
525	GTCGAAGCCAGGAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	584			
616	CCCTCTCTCTACATCTACATCTACATCTACATCTACATCTACATCTACATCTAC	675			
585	CCCTCTCTCTACATCTACATCTACATCTACATCTACATCTACATCTACATCTAC	637			
676	AGGGGAGATGAGAGATGAGAGATGAGAGATGAGAGATGAGAGATGAGAGATGAG	735			
638	-----GGAGGATGAGAGATGAGAGATGAGAGATGAGAGATGAGAGATGAGAG	689			
736	TTCAATTCAGCAT	795			

Db		690	TCCAGTTCACAGACATCATGATGGGTCTCATTCCCGCGGGGCATGCTATCTGTCCTGCT	749
Oy		796	ACTGCATCATCATCTC 811 	
Db		750	ACTGCATCATCATCTC 765	
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	DEFINITION	U75A01.y1 Soares_mouse_MNGB.bcell Mus musculus cDNA clone IMAGE:3333409 5' similar to SW:CCR4_MOUSE P70658 C-X-C CHEMOKINE RECEPTOR type 4 ; mRNA sequence.		
	ACCESSION	BGI45042		
	VERSION	BGI45042.1	GI:12648446	
	KEYWORDS	EST.		
	SOURCE	house mouse.		
	ORGANISM	Mus musculus		
	REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
	AUTHORS	NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.		
	TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index Unpublished (1997)		
	JOURNAL	Contact: Robert Strausberg, Ph.D.		
	COMMENT	Email: csapbs-rfemail.nih.gov This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -40RP from Gibco MG1:107573		
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		/lab_host="DH10B (phage-resistant)"		
		/note="Organ: germinal B-cell; Vector: p773D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTACCAATCTGAAGTGAGCGCGCGCGTGTGTTTTTTTTTTTTTTTTTTTTTTT 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested w/ht Not I and cloned into the Not I and Eco RI sites of the modified p773 vector. Library is normalized; constructed by Bento Soares and M.Feliana Bonaldo."		
	COUNT	123 a 184 c 129 g 145 t 1 others		
	ORIGIN			
	Query Match	29.4%	Score 551.6;	DB 12; Length 582;
	Best Local Similarity	98.1%;	Pred. No. 5.2e-57;	
	Matches 568:	Conservative 0;	Mismatches 10;	Indels 1; Gaps 1;
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Oy		672	AGTCAGGGGGATGACAGGTACATCTGTGACCCTTTAACCCGATVAGCTGTGGATGATG	731
Db		61	AGTCAGGGGGATGACAGGTACATCTGTGACCGCTTTAACCCGATVAGCTGTGGATGATG	120
Oy		732	GTCGTTCAATTCCAGCATATATGTTGGGCTCATCTCCGCCGCATGTCATCTCTCC	791
Db		121	GTCGTTCAATTCCAGCATATATGTTGGGCTCATCTCCGCCGCATGTCATCTCTCC	180
Oy		792	TGTTACGTCATCATCTCTTAACCTGTCAACATCCAAAGGGCCACCAAGCCGAAGGCC	851
Db		181	TGTTACGTCATCATCTCTTAACCTGTCAACATCCAAAGGGCCACCAAGCCGAAGGCC	240

QY	852	CTCAAGACAGCATATCTCATCTATCTTCTTGGCTGCTGCATATTAATG	911
Db	241	CTCAAGACAGCATATCTCATCTTCTTGGCTGCTGCATATTAATG	300
QY	912	GGGATCAGCATGACTCTTCTTGGAGTCAATCAAGCAAGATGTGACTGAG	971
Db	301	GGGATCAGCATGACTCTTCTTGGAGTCAATCAAGCAAGATGTGACTGAG	360
QY	972	AGCATTTGTCACAAAGTGATTCATTCACAGAGGCGCTTCTTCTTGGCTG	1031
Db	361	AGCATTTGTCACAAAGTGATTCATTCACAGAGGCGCTTCTTCTTGGCTG	420
QY	1032	AAACCATCTCTATGCGCTTCTTGGAGGCGCAAGTTCAAAAGCTGCGCCACATGACATC	1091
Db	421	AAACCATCTCTATGCGCTTCTTGGAGGCGCAAGTTCAAAAGCTGCGCCACATGACATC	480
QY	1092	AACCTCATGACAGAGGCTCCAGGCTCAAGATCTTTCCAAAGAAAGGAGGAGTGCACAC	1151
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DEFINITION	603046395F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5186878 5',		
ACCESSION	B1761664		
VERSION	B1761664.1	GI:15753242	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
TITLE	1 (bases 1 to 827)		
JOURNAL	NIH-MGC http://mgc.nci.nih.gov/.		
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)		
	Contact: Robert Strausberg, Ph.D.		
	Email: cs9abs-remail.nih.gov		
	Tissue Procurement: Life Technologies, Inc.		
	cDNA Library Preparation: Life Technologies, Inc.		
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)		
	DNA Sequencing by: Incyte Genomics, Inc.		
	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:		
	http://image.lnl.gov		
	Plate: L14M11466 row: m column: 23		
	High quality sequence stop: 827.		
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	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
	/clone="IMAGE:5186878"		
	/clone_lib="NIH_MGC_116"		
	/lab_host="DH10B"		
	/note="Organ: pooled colon, kidney, stomach; Vector: PCWV-SHORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 3 colons, age 26 yo male, 49 yo female, 71 yo male colon; 46 yo male kidney, and pool of 2 stomachs, 62 yo male and 70 yo female. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 023. Note: this is a NIH_MGC Library."		
BASE COUNT	190 a 232 c 194 g 210 t	1	others

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 12, 2003, 15:03:23 ; Search time 235 Seconds
(without alignments)
12611.805 Million cell updates/sec

Title: US-09-367-052-1

Perfect score: 1877

Sequence: 1 ccatcctaatacactactact.....aaaaaaaaaaaaaaaaaa 1877

Scoring table: IDENTITY_NIC

Gapop 10.0 , Gapext 1.0

Number of hits satisfying chosen parameters: 2210862

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: Published Applications - NA *

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	974.4	51.9	1737	9 US-09-104-063-3	Sequence 3, Appl1
2	952.8	50.8	1679	9 US-10-225-567A-75	Sequence 75, Appl1
3	944.8	50.3	1670	10 US-09-880-107-2143	Sequence 2143, Ap
4	808	43.0	1102	9 US-09-870-759-143	Sequence 143, App
5	576.4	30.7	1902	10 US-09-953-692-1	Sequence 1, Appl1
6	576.4	30.7	1902	10 US-09-953-692-1	Sequence 1, Appl1
7	303.2	16.2	421	9 US-09-796-692-2611	Sequence 2611, Ap
8	303.2	16.2	421	9 US-10-040-862-2611	Sequence 2611, Ap
9	287	15.3	487	9 US-09-796-692-8936	Sequence 8936, Ap
10	287	15.3	487	9 US-10-040-862-8936	Sequence 8936, Ap
11	198.4	10.6	1119	9 US-10-251-385-65	Sequence 65, Appl1
12	198.4	10.6	1119	9 US-09-104-063-5	Sequence 5, Appl1
13	198.4	10.6	1119	9 US-10-225-567A-59	Sequence 59, Appl1
14	196.8	10.5	1119	9 US-10-251-385-199	Sequence 199, App
15	193.8	10.3	1107	9 US-10-251-385-19	Sequence 19, Appl1
16	193.8	10.3	1670	9 US-10-225-567A-73	Sequence 73, Appl1
17	193.8	10.3	1670	10 US-09-880-107-383	Sequence 383, Ap
18	193	10.3	1877	9 US-10-106-698-2125	Sequence 2125, Ap
19	192.2	10.2	1107	9 US-10-251-385-173	Sequence 173, App

20	188.8	10.1	1068	9 US-10-237-563-45	Sequence 45, Appl1
21	185	9.9	1068	9 US-10-237-563-47	Sequence 47, Appl1
22	182.8	9.7	1068	9 US-10-237-563-43	Sequence 43, Appl1
23	182.8	9.7	1068	9 US-10-237-563-44	Sequence 44, Appl1
24	182	9.7	1137	9 US-10-251-385-73	Sequence 73, Appl1
25	182	9.7	2139	9 US-10-225-567A-67	Sequence 67, Appl1
26	181.4	9.7	1068	9 US-10-237-563-48	Sequence 48, Appl1
27	181.4	9.7	1074	9 US-10-237-563-23	Sequence 23, Appl1
28	181.4	9.7	2462	9 US-10-225-567A-240	Sequence 240, App
29	181.4	9.7	2577	9 US-09-966-755-1	Sequence 1, Appl1
30	181.4	9.7	2577	10 US-09-903-377-1	Sequence 1, Appl1
31	181.4	9.7	2577	10 US-09-952-385-1	Sequence 1, Appl1
32	181.4	9.7	2577	12 US-10-000-759A-1	Sequence 1445, Ap
33	180.4	9.6	1318	10 US-09-917-800A-1445	Sequence 15, Appl1
34	179.8	9.6	2050	9 US-09-940-240-15	Sequence 42, Appl1
35	179.6	9.6	1068	9 US-10-237-563-42	Sequence 462, App
36	179.6	9.6	2496	9 US-10-225-567A-462	Sequence 203, App
37	178.8	9.5	1137	9 US-10-251-385-203	Sequence 175, App
38	178.2	9.5	1074	9 US-10-251-385-175	Sequence 41, Appl1
39	178	9.5	1068	9 US-10-237-563-41	Sequence 1, Appl1
40	178	9.5	1933	9 US-09-104-063-1	Sequence 46, Appl1
41	177.8	9.5	1068	9 US-10-237-563-46	Sequence 385, App
42	177.8	9.5	2856	9 US-10-225-567A-385	Sequence 38, Appl1
43	176.2	9.4	1068	9 US-10-237-563-38	Sequence 40, Appl1
44	173	9.2	1053	9 US-10-237-563-40	Sequence 627, App
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ALIGNMENTS

RESULT 1
US-09-104-063-3
Sequence 3, Application US/09104063
Patent No. US20020168356A1
GENERAL INFORMATION:
APPLICANT: Lee, James
TITLE OF INVENTION: PF4A Receptors
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/104,063
FILING DATE: 24-June-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: -08/701265
FILING DATE: 22-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/664228
FILING DATE: 06-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/076093
FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/810782
FILING DATE: 19-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P0706P2C2
TELECOMMUNICATION INFORMATION:

TELEPHONE: 415/252-5530
TELEFAX: 415/955-9881
TELEX: 910/371-7168
INFORMATION FOR SER ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 1737 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
US-09-104-063-3

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Best Local Similarity	76.1%	Pred. No. 4.7e-220;		
Matches 1301; Conservative	0;	Mismatches 301;	Indels 136;	Gaps 10;

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Db	1684	AAAAAAAAAAAAAAAAAAAAAAAAA	1711

RESULT 2
US-10-225-567A-75
; Sequence 75, Application US/1022556775
; Publication No. US20030112798A1
; GENERAL INFORMATION:
; APPLICANT: Lifespan Biosciences

APPLICANT: Brown, Joseph P.
APPLICANT: Burner, Glenna C.
APPLICANT: Roush, Christine L.
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 1920-4-4
CURRENT APPLICATION NUMBER: US/10/225,567A
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/257,144
PRIOR FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 2292
SOFTWARE: PatentIn version 3.1
SEQ ID NO 75
LENGTH: 1679
TYPE: DNA
ORGANISM: Homo sapiens
US-10-225-567A-75

Query Match 50.8%; Score 952.8; DB 9; Length 1679;

Best Local Similarity 80.2%; Pred. No. 5,9e-215;

Matches 1210; Conservative 0; Mismatches 252; Indels 46; Gaps 6;

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164 TGAAGAGTGGGGTGTGAGACTATGATCAACAAGAACCTGCTCCGGAGTAAAA 223
127 CGAGAAATGGGCTCAGGGGACTATGATCAATGAAGAACCTGTTCCGTAAGAAA 186
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1466 TATGATA 1473

RESULT 3
US-09-880-107-2143.
Sequence 2143, Application us/09880107
Patent No. US20020142981A1
GENERAL INFORMATION:
APPLICANT: Horne, Darci T.
APPLICANT: Vockley, Joseph G.
APPLICANT: Scherf, Uwe
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
FILE REFERENCE: 44921-5028-WO
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: US 60/237,054
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2143

LENGTH: 1670
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Genbank Accession No. US20020142981A1 L06797
US-09-880-107-2143

Query Match 50.3%; Score 944.8; DB 10; Length 1670;
Best Local Similarity 75.9%; Pred. No. 4,6e-213;
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D 553 TGGATGCCAGCCCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 601
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D 602 -----TCAGTGGAGGAGATGACAGTGTGATGAGCGCTTACCCGATAGGCTGTG 657
QY 726 ATGTGTGTGTTCATTCAGCATATATATGTGGGTCTGCTGCTGCTGCTGCTGCTGCTGCT 785
D 658 GTGTGTGTGTTCATTCAGCATATATATGTGGGTCTGCTGCTGCTGCTGCTGCTGCTGCT 717
QY 786 CTCTCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 845
D 718 CTCTCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 777
QY 846 AAGGCCCTCAAGAGCAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 905
D 778 AAGGCCCTCAAGAGCAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 837
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D 838 TATGTGGGATGAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 897
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D 898 TTGGAAGCATTTGTGCAAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGAT 957
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QY 1086 GCACCTCAACCTCCATGAGCAGAGGCTCCAGCCCTCAAGATCTCTTCCAAAGAAAGCGGGCT 1145
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D 1132 --CACAGATGTAGAGACTTTTATATATATATATATATATATATATATATATATATATAT 1189
QY 1266 TTCCAGATATAGAGACTGACAGCAGTCTGTACAGTCTTCTTCTTCTTCTTCTTCTTCTTCT 1325
D 1190 TTCCAGATATAGAGACTGACAGCAGTCTGTACAGTCTTCTTCTTCTTCTTCTTCTTCTTCT 1245
QY 1326 GGGAGTTATATGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1385
D 1246 TGCCTCTGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1302
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D 1303 TTTTCTGTTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1362
QY 1446 TTTATCTGTGTAGAGACTGTAGAACTGTAGAGAAAGAAATTCAGATGATGATGATGATGAT 1505
D 1363 TATGCTGCTGTAGAGACTGTAGAA-----AAGGCACTGATGATGATGATGATGATGATGAT 1414
QY 1506 GGTAAATGATTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1565
D 1415 AGTGAATGATTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1473
QY 1566 AGGAGACCCACCCACCCACCCACCCACCCACCCACCCACCCACCCACCCACCCACCCACCCAC 1625
D 1474 ----- 1473
QY 1626 GTGATGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTT 1685
D 1474 -----TTCCCGTGAAGCTTTTCTGTTTCTTGAAGAGTATGTTTCTGTGAAGAGT 1526
QY 1686 GCACCTTAACCAAGCCGTAAGTGTGTAAGTGTGTAAGTGTGTAAGTGTGTAAGTGTGTAAGTGT 1745
D 1527 GCACCTTAACCAAGCCGTAAGTGTGTAAGTGTGTAAGTGTGTAAGTGTGTAAGTGTGTAAGTGT 1566
QY 1746 TTTTCTGATGTTTCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1805
D 1567 -TTTTCTGATGTTTCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1624
QY 1806 CATGTTAATTAAGTCAATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1851
D 1625 AGTGTATTAATTAAGTCAATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1670
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RESULT 4
US-09-870-759-143
Sequence 143, Application US/09870759
Patent No. US20020177551A1
GENERAL INFORMATION:
APPLICANT: TERMAN, David S
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
FILE REFERENCE: 870759
CURRENT APPLICATION NUMBER: US/09/870,759
CURRENT FILING DATE: 2002-01-14
PRIOR APPLICATION NUMBER: US 60/208,128
PRIOR FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 166
SOFTWARE: PatentIn version 3.1

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: SEQ ID NO 143
:
: LENGTH: 1102
:
: TYPE: DNA
:
: ORGANISM: Homo sapiens
:
: FEATURE:
:
: NAME/KEY: CDS
:
: LOCATION: (44)..(1102)
:
: OTHER INFORMATION:
:
: US-09-870-759-143

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Query Match	43.0%;	Score 808;	DB 9;	Length 1102;
Best Local Similarity	85.9%;	Pred. No. 7.7e-181;		
Matches 914;	Conservative 0;	Mismatches 135;	Indels 15;	Gaps 1

[illegible]

RESULT 5
US-09-953-692-1

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; LOCATION: (158) (223) (225) (226) (335) (466) (520) (530) (645) (763) (825) (1120)
; LOCATION: (1183)
US-09-953-692-1

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QY	44	GCAGGTGACAGTAGCAGTGAACCTCTGAGCGCTTTGGTCTCCGGTAACCAACACGCGTG	103
Db	12	GCGGCAGCAGTAGCAGCAAGTAGCACGCCGAGGCGCTGAGTGCCTCAGATACACCCGATCTG	71
QY	104	TAGAGCGAG-TGTTGCCATGTGAACCGATGAGTGTATATACCTCTGTATACTACT	162
Db	72	GAGAACCCAGCGTTACATGGAGGGATCTM-----GAGTATATACCTTACAGTATACATA	127
QY	163	CTGAAGAAGTGGGCTGTGGAGACTA-----TGACTTCAACAAGAACCCGTG	208
Db	128	CCGAGGAATGGGCTCAGGGGACTASYSNDNTWMSGDTGTACTCATGAAGAACCCGTG	187
QY	209	CTTCCGGATGAANAAGTCCTATTTCAATAG-----ATCTCTGCCACCACTCT	258
Db	188	TTTCCGTAAGAAATAATGCTAATTTTCAATAADSMKCRNANNAATCTCTCCGCCACACTCT	247
QY	259	ACTTCATGATCTTCTTGACTGGCATAGT-----CGCAATGATGTGGTATCTCTGGTC	311
Db	248	ACTCATATATCTTTCTTAAGCTGGCATTTGKTYSTGVGCCAATGATTTGGTATCTCTGGTC	307
QY	312	ATGGGTTACCAAGAAAGACTAAG-----GAGCATGACGAGCAAGTACCGCGTG	359
Db	308	ATGGGTTACCAAGAAAGAACTGAGAGGNGVWYKRSOATGACGAGCAAGTACAGCGCTG	367
QY	360	CACCTGTAGTGTGCTGACTCTCTTTTG-----TATACACTCCCTCTCTGGG	408
Db	368	CACCTGTAGTGTGCGACTCTCTTTTGTDRYRHSVADTATATCATACGCTTCTCCCTTCTGGG	427

OY	409	AGATTGATGCCATGGCTACAGTGGATCACTT-----GGGAAATTTTGGTGAAG	456
Db	428	CAGTTGATGCCGTGGCAACACTGGTACTTTTVMVADANVMGGGAACTTCTTATGCAAG	487
OY	457	CTGTCCATATCATGTACACTGTCAACCTCTA-----CAGCAGCGTTTCTCATC	503
Db	488	CAGTCCATGTCTATGTACACATCAACCTCTAGNCKAHVTVNNCAGCAGATGTCTCATC	547
OY	504	CTGGCCTTATCAGCCTTGGACCGGTACTGGCC-----ATTGTCCAGCCAGCAAC	554
Db	548	CTGGCCTTATCAGCTGTGGACCGGTACTGGCCASVSADRYATGTCTCAGCCAGCAAC	607
OY	555	AGTCAAAAGGCCAAGAAACTGTGGCTTAAAGGA-----GTATATGGGGCG	603
Db	608	AGTCAAGAGGCCAAGAAAGCTTTGGCTGTAAAGVNIATSKRKAGTGGTCTATGTGGCG	667
OY	604	TCTGGATCCAGCCCTCTCTCTGACTATACCTTATCTTGGCCAGCTCAAGCCAG	663
Db	668	TCTGGATCCAGCCCTCTCTCTGACTATTCGCAVYVYGVAT-----DCTCATCTTGG	722
Db	664	GGGACATCAGTCAGGGGGATGACAGAGTACATCTGTGACC-----GCCTTACCC	712
Db	723	CCAACGTGAGGAGGCAAGATACAGATATATCTGTGACCAVMSADRYRCDCTTCTACCC	782
OY	713	CGATAGCCTGTGAAATGGTGGTGTTCATATCCAGATAT-----AAGTGGGGCT	763
Db	783	CAATGACTTGTGGGGTGTGTGTTCATATTCAGCATCGRYNDMVUVAHGGTGGCT	842
OY	764	CATCTCGCCCGGCACTGTCAATCTCTCTGTGTACTGATC-----ATCATCTCTAA	814
Db	843	TATCTGGCTGTGTATTTGATCTCTGTCTGTCTATTCATATMGVSYCTATCATCTCAA	902
OY	815	GCTGTACACTTCCAAAGGGCCACAGAAAGCAAGGCC-----TCAAGACAG	862
Db	903	GCTGTCAACTTCCAAAGGGCCACAGAAAGCAAGGCCSKSHKMKRKATCAAGACAC	962
OY	863	AGTATCTCAATCCAGCTTCTTGGCTGTGGCTG-----CATATATCTGGG	914
Db	963	AGTATCTCAATCCAGCTTCTTGGCTGTGGCTGTGTAAACATCTACATTTGG	1022
OY	915	ATCAGCATCGACTCTTTCATCTTTTGGGATCATCAA-----GCAGAGTGTGACTT	967
Db	1023	ATCAGCATCGACTCTTTCATCTCTCTCTGGAATCATCAAYPSDSKCAAGGCTGTGACTT	1083
OY	968	CGAGAGCATTTGCAACAAGTGATCTCATACAG-----AGCCCTCGCTTCT	1017
Db	1083	TGAGAGCACTGTGCACAAGTGATTTCCATCACGGGCTVHKMSTAGCCCTTACTTCT	1142
Db	1018	TTCACCTGTGGCTAAACCCCATCTCTATGGCTTC-----CTGGGGGCCAAGTCTAA	1065
Db	1143	TTCACCTGTGTGTAAACCCCATCTCTATGGCTTCAAHNCVACTTGGAGCAAATTTTAA	1202
OY	1070	AAGCTCTCCAGCATGCACTCAACTC-----CATGAGCAGAGGCTCCAGCC	1118
Db	1203	AACCTCTCCAGCAGCAGCACTCACTCTGTAGAGAKTSAHATVSYSCAGAGGCTCCAGCC	1266
OY	1117	TCAGATTCCTTCCAAAGGAAAGGGGGTGACACT-----CTTCCGTCTCC	1163
Db	1263	TCAGATTCCTTCCAAAGGAAAGGAGGTGACATTTRESSKSKRGHCACTGTCTCC	1322
OY	1164	ACGAGATCAGAAATCTCCAGTTTTCACTCAGCTA--ACCCTTATGCAAAACCTTATATA	1221
Db	1323	ACTGAGTGTGAGTCTTCAAGTTTTCACTCAGCTCAACSSVTSSSHASAGATGTAA	1382
OY	1222	ATATATATATATATGATTAAGAACTTTTAT--GTATACAAATTTCCAGATATAGA	1279
Db	1383	AGACTTTTATATATGATTAAGATTAACCTTTTATTTAAGTTACAGATTTTCCAGATTAATA	1442
OY	1280	GACTGACCAAGTCTGTACAGTTTTTTTTTTTTTAAATGACGTGGAGATTTATGTTC	1339
Db	1443	GACTGACCAATATTTGTACAGTTTTTATTTGCTTTGGATTTTTGG-----CTTGTGTTT	1498
OY	1340	CTGTAGTTTTTGTAGAGTTTGACTTAATTTATTAATATATGTTTTTTGTTTTGTTTCATG	1399

Query	Match	30.7%	Score 576.4	DB 10	Length 1902
Db	1497	CTTTAGTTTGTGTAAGTTTAATGACTTATTATTA	-----	TAATTTTTTTTGTGTCATA	155
QY	1400	TGAATGAGCGTCTAGGACGAGCACTGTGGCCAA	TTCTTAGTACCTGTTTATCTGTGTGA	1455	
Db	1553	TTGATGTGTCTAGGACGAGCACTGTGGCCAA	TTCTTAGTGTGTGTCTGTGTGTGA	1612	
QY	1460	GGACTGTAGCACTGTAGAGGAAAGCAATCCGAA	TTCCGAAATGTGTGTAAATTAATTA	1519	
Db	1613	GGACTGTAGAA-----	AAGGAGACGAAACATTCCAGACGCTGTAGTCAATACGCTAA	1664	
QY	1520	AGCTAGCGGTATCCTCAGCTGTGCTGCATA	1551		
Db	1665	AGCTAGAAATGATCCCGACGCTGTTTATGCATA	1696		
RESULT 6					
US-09-953-717-1					
Sequence 1, Application US/09953717					
Patent No. US20020107196A1					
GENERAL INFORMATION:					
APPLICANT: Shalley, Gupta K.					
TITLE OF INVENTION: Method for Inducing Chemotaxis in Endothelial Cells by					
TITLE OF INVENTION: Administering Stromal Cell Derived Factor-1					
FILE REFERENCE: P50676D1					
CURRENT APPLICATION NUMBER: US/09/953,717					
CURRENT FILING DATE: 2001-09-17					
PRIOR APPLICATION NUMBER: 09/358,624					
PRIOR FILING DATE: 1999-07-21					
PRIOR APPLICATION NUMBER: 60/093,596					
PRIOR FILING DATE: 1998-07-21					
NUMBER OF SEQ ID NOS: 6					
SOFTWARE: FastSeq for Windows Version 3.0					
SEQ ID NO 1					
LENGTH: 1902					
TYPE: DNA					
ORGANISM: Human					
FEATURE:					
NAME/KEY: unsure					
LOCATION: (158)(223)(225)(226)(335)(466)(520)(530)(645)(763)(825)(1120)					
LOCATION: (1183)					
US-09-953-717-1					
Query Match					
Best Local Similarity 70.8%; Pred. No. 6.4e-126;					
Matches 1212; Conservative 26; Mismatches 243; Indels 231; Gaps 27					
QY	44	GCAGGTGAGGTAGCAGTACGACCTCTGAGGGGTTGTGTC	CCGGTAAACACACAGCGCTG	103	
Db	12	GGCGGAGGAGTAGAAGTAGACGCGGAGGCGCTGAGTGTCT	CACTAGCAGCGCATCTG	71	
QY	104	TAGAGCGAG-TGTTGCCATGGAACCGATGAGTATATAC	ACTTCTGATACTACT	162	
Db	72	GAGAACCGCGCGTATACCACTGAGAGGGATCM----	GAGATATACACTTCAGATACATACATA	127	
QY	163	CTGAAGAAAGTGGGTCTGGAGACTA-----	TGACTCAAGAAAGACCTG	208	
Db	128	CCGAGGAATGGGCTCAGGGGACTASYS	SDNYTMGSDYTGACTCCATGAAAGAACCTG	187	
QY	209	CTTCCCGGATTAATAACCTTCATTAAG-----	ATCTCTCGCCCAACCACT	258	
Db	188	TTTCCGTAAGAAATAATGCTAATTTCAATADSMKCR	NANNAATCTTCTGCGCCACATCT	247	
QY	259	ACTTCATCATTTCTTGACTGGCATAGT-----	CGGCAATGATTTGGTATCCGTG	311	
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QY	360	CACCTGTACGTGGCTGACCTCTCTTGG-----	TCATCACACTCCCTCTTGTGG	408	

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Db 368 CACGTGTCAGTGGCCGACCTCCTCTTGTGMDTKYRHVSADTCATCAGCTTCCCTCTGG 427
QY 409 CAGTTGATGCATGGCTGACTGTACTTT-----GGGAATTTTGTGTAGG 456
Db 428 CAGTTGATGGCCGTGCAACCTGTACTTTVWADVAMVWGGAGACTTCCATCAAGG 487
QY 457 CTGTGCATATCATCTACACCTGTCAACCTCTA-----CAGCAGCTTGTATC 503
Db 488 CAGTGCATGTCTATCAGACAGTCAACCTGTAGNCKAIVHYVYNYCAGCAGTCTCTATC 547
QY 504 CTGGCTTCATCAGCTGTGACCGGTACTCTGCGC-----ATTGTCACGCCACCAAC 554
Db 548 CTGGCTTCATCAGCTGTGACCGGTACTCTGCGCASSVADRYATGTCACGCCACCAAC 607
QY 555 AGTCAAGGCCAAGAACTGTGGCTGAAAAGCA-----GTCTATGTGGGCG 603
Db 608 AGTCAGAGGCCAAGAACTGTGGCTGAAAAGVATNSRRKAKGTGTGTGTGGGCG 667
QY 604 TCTGATCCCAAGCCCTCTCTGACTATACCTGATCTCTTTCGCGACGTCAAGCAG 663
Db 668 TCTGATCCCTGCTCTCTGCTGACTATTCGCGAIVYGVAT-----DCTTCATCTTGG 722
QY 664 GGGACATAGTCAGGGGATGACAGGTACATCTGTACC-----GCTTTTACC 712
Db 723 CCAACGTGATGAGGCGAGATGACAGATATCTGTGACCANYSADRYCDGCTCTACCC 782
QY 713 CGATGCGTGGATGTGTGTCTTCAATCCAGCATAT-----AATGCTGGGCT 763
Db 783 CAATGCTGTGGGTGTGTGTGTCTTCAAGTTCAGACATCRYNDVWVHATGTGGGCT 842
QY 764 CATCTGCGCGGATCTGATCTCTCTGTACTGATC-----ATGATCTTAA 814
Db 843 TATCTGCTGTGTATGTGATCTCTCTGCTATGTCATMVGVCYCATATCTCCAA 902
QY 815 GCTGTACACTCCAAAGGCCACAGAGGCCAGGCC-----TCAAGACGAC 862
Db 903 GCTGTACACTCCAAAGGCCACAGAGGCCACCCSKSHKGRKATCAAGACAC 962
QY 863 AGTCATGCTCATCTGAGCTTCTTGGCGTGGGCTGC-----CATATATGTGGG 914
Db 963 AGTCATCTCATCTGAGCTTCTTGGCGTGGGCTGCTTVAACWATCACTACATGGG 1022
QY 915 ATCAGCATGACTCTCTTATCTCTTGGAGTCAATCA-----GCAAGATGTGACT 967
Db 1023 ATCAGCATGACTCTCTTATCTCTCTGGAATCAATCAIYSDSGCAAGGTGTGAGTT 1082
QY 968 CGAGCAGATGTGCACAAAGTGTCTCATCAGAC-----AGGCCCTGCGCTTCT 1017
Db 1083 TGAGAACACTGTGCACAAAGTGTCTCATCACCGGCMVHKWSTAGGCCCTAGCTTCT 1142
QY 1018 TCCACTGTGTGCTGAACCCATCTCTATGCTTC-----CTCGGGGCCAAGTTCA 1069
Db 1143 TCCACTGTGTGTGAACCCATCTCTATGCTTCAAHCCNACTTGGAGGCCAATTTAA 1202
QY 1070 AAGCTGTGCCAGCATGACTCACTC-----CATGAGCAGAGCTCCAGCC 1116
Db 1203 AACCTGTGCCAGCAGCATCACTCTGTGAGAKKTSAHNTSVSCAAGAGTCCAGCC 1262
QY 1117 TCAAAATCTTTTCCAAAGAAAGCGGGTGAACCT-----CTTCCCTTCC 1163
Db 1263 TCAAAATCTTTTCCAAAGAAAGCGAGTGCACATTTGSSSKRGHCATCTCTTCC 1322
QY 1164 ACGGAGTGAAGTCTTCCAGTTCATCTCCAGCTA--ACCTTATGCAAGACTATATA 1221
Db 1323 ACTGATCTGAGTCTTCAAGTTCATCTCCAGCTAACSSVSTSSSSSSAGATGTAA 1382
QY 1222 ATATATATATATATATGAAGAACTTTTAT--GTTACATTTTCCAGATATAGA 1279
Db 1383 AAGCTTTTATATAGATATATATCTTTTATTTTAAAGTACACATTTTCCAGATATAGA 1442
QY 1280 GACTGACCAAGTCTGTGACAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1339
Db 1443 GACTGACCAAGTCTGTGACAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1496
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QY 1340 CTCTAGTTTTGTAGGTTTGACTTAATTTATATATATTTGTTTTGTTTCTCANG 1399
Db 1497 CTTTATGTTTTGTGAGTTTAAATTTATGACTTATTATTA-----TAAATTTTTTGTTCATA 1552
QY 1400 TGAATGACCGTCTAGGACGAGACCTGTGGCAAGTCTTACTAGTGTATTACTGTGTGA 1459
Db 1553 TTGATGTGTGTAGGACGAGACCTGTGGCAAGTCTTACTAGTGTATTACTGTGTGA 1612
QY 1460 GGACTGTGAACTGTGAGAGGAAGAACTGAACATTTCCAGATGTGTGTAAATTTGAATPA 1519
Db 1613 GGACTGTGAA-----AAGGGAACAGCAATTCAGAGCGGTGTAGTGAATCAGTAA 1664
QY 1520 AGCTAGCCGTGATCTCTGACGCTGTGCTGATA 1551
Db 1665 AGCTAGAAATGATCCCAAGCTGTATTATGATA 1696

RESULT 7
US-09-796-692-2611
; Sequence 2611, Application US/09796692
; Public Information No. US20020198362A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Manion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THER
; FILE REFERENCE: 2077.001200
; CURRENT APPLICATION NUMBER: US/09/796,692
; CURRENT FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,378
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 9597
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2611
; LENGTH: 421
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-796-692-2611

Query Match 16.2%; Score 303.2; DB 9; Length 421;
Best Local Similarity 83.3%; Pred. No. 9,4e-62;
Matches 363; Conservative 0; Mismatches 58; Indels 15; Gaps 1;

QY 547 CCACCAACGCTGAAGGCCAAGAAAGCTGTGCTGAAGAAAGCGATGAGGCGCT 606
Db 1 CCACCAACGCTGAAGGCCAAGAAAGCTGTGCTGAAGAAAGCGATGAGGCGCT 60
QY 607 GGATCCCAAGCCCTCTCTGACTATACCTGACTTATCTTTTCCGACGTCAAGCGG 666
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Db 61 GGATCCCTGCCCCCTCTGCTGACTATATCCCGACTTCATCTTGCCNAGC----- 108
OY ACATGAGTCAGGGGATGACAGGTACATCTGTGACCGGCTTACCCGATAGCCGTGGA 726
Db 109 ---TCAGTAGGACATACAGATATATCTGTGACCGGCTTACCCGATAGCTTGTGG 165
OY 727 TGTGTGTTTCATATCCAGCATATATATGTGGTCTCTATCTGCGCCGCAATCGTCATCC 786
Db 166 TGGTGTCTTCCAGTTTACGACATCATGTGTGGCTTATCTGCTGTGTATGTGCATCC 225
OY 787 TCTCTGTACTGATCATCATCTTATAGCTGTACATCCAGGGCCACAGAGGCCA 846
Db 226 TGTCTGTATGTATTCATCTTCAAGCTGTACACTCCAGGCGCCACAGAGGCCA 285
OY 847 AGGCCCTCAAGACAGCATCTCTCATCTAGCTTTTGTGCGCTGTGCGGCATATTT 906
Db 286 AGGCCCTCAAGACAGCATCTCTCATCTAGCTTTTGTGCGCTGTGCGGCATATTT 345
OY 907 ATGTGGGATGACATGCTCTCTTCATCTTTTGGAGTCAATCAAGAGATGTGACT 966
Db 346 ACATGGGATGACATGCTCTCTTCATCTCTCGAATATCATCAAGAGGTTGTGAGT 405
OY 967 TCGAGAGCATTTGTGCA 982
Db 406 TTGAGAACACTGTGTGCA 421

RESULT 8

US-10-040-862-2611

Sequence 2611, Application US/10040862

Publication No. US20030078396A1

GENERAL INFORMATION:

APPLICANT: Gaiger, Alexander

APPLICANT: Algate, Paul A.

APPLICANT: Mannion, Jane

APPLICANT: Retter, Marc

APPLICANT: Corixa Corporation

TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy

FILE REFERENCE: 014058-013520US

CURRENT APPLICATION NUMBER: US/10/040,862

CURRENT FILING DATE: 2001-11-06

PRIOR APPLICATION NUMBER: US 60/186,126

PRIOR FILING DATE: 2000-03-01

PRIOR APPLICATION NUMBER: US 60/190,479

PRIOR FILING DATE: 2000-03-17

PRIOR APPLICATION NUMBER: US 60/200,545

PRIOR FILING DATE: 2000-04-27

PRIOR APPLICATION NUMBER: US 60/200,303

PRIOR FILING DATE: 2000-04-28

PRIOR APPLICATION NUMBER: US 60/200,779

PRIOR FILING DATE: 2000-04-28

PRIOR APPLICATION NUMBER: US 60/200,999

PRIOR FILING DATE: 2000-05-01

PRIOR APPLICATION NUMBER: US 60/202,084

PRIOR FILING DATE: 2000-05-04

PRIOR APPLICATION NUMBER: US 60/206,201

PRIOR FILING DATE: 2000-05-22

PRIOR APPLICATION NUMBER: US 60/218,950

PRIOR FILING DATE: 2000-07-14

PRIOR APPLICATION NUMBER: US 60/222,903

PRIOR FILING DATE: 2000-08-03

PRIOR APPLICATION NUMBER: US 60/223,416

PRIOR FILING DATE: 2000-08-04

PRIOR APPLICATION NUMBER: US 60/223,378

PRIOR FILING DATE: 2000-08-07

PRIOR APPLICATION NUMBER: US 09/796,692

PRIOR FILING DATE: 2001-03-01

NUMBER OF SEQ ID NOS: 10467

SOFTWARE: FASTSEQ for Windows Version 3.0

SEQ ID NO 2611

LENGTH: 421

TYPE: DNA

ORGANISM: Homo sapiens
US-10-040-862-2611

Query Match 16.2%; Score 303.2; DB 9; Length 421;

Best Local Similarity 83.3%; Pred. No. 9,4e-62;

Matches 363; Conservative 0; Mismatches 58; Indels 15; Gaps 1;

OY 547 CCACCAACAGTCACCAAGGCAAGAACGCTGCGGTGAAAGGACAGTATATGTGGCGCT 606
Db 1 CCACCAACAGTCACCAAGGCAAGAACGCTGCGGTGAAAGGACAGTATATGTGGCGCT 60
OY 607 GGATCCAGCCCTCTCTGCTGACTATACCTGACTTATCTTATGCGAGCTGACGAGGGG 666
Db 61 GGATCCAGCCCTCTCTGCTGACTATACCTGACTTATCTTATGCGAGCTGACGAGGGG 108
OY 667 ACATGAGTCAGGGGATGACAGGTACATCTGTGACCGGCTTACCCGATAGCCGTGGA 726
Db 109 ---TCAGTAGGACATACAGATATATCTGTGACCGGCTTACCCGATAGCTTGTGG 165
OY 727 TGTGTGTTTCATATCCAGCATATATATGTGGTCTCTATCTGCGCCGCAATCGTCATCC 786
Db 166 TGGTGTCTTCCAGTTTACGACATCATGTGTGGCTTATCTGCTGTGTATGTGCATCC 225
OY 226 TGTCTGTATGTATTCATCTTCAAGCTGTACACTCCAGGCGCCACAGAGGCCA 285
OY 286 AGGCCCTCAAGACAGCATCTCTCATCTAGCTTTTGTGCGCTGTGCGGCATATTT 906
Db 346 ACATGGGATGACATGCTCTCTTCATCTCTCGAATATCATCAAGAGGTTGTGAGT 405
OY 346 ACATGGGATGACATGCTCTCTTCATCTCTCGAATATCATCAAGAGGTTGTGAGT 405
OY 907 ATGTGGGATGACATGCTCTCTTCATCTTTTGGAGTCAATCAAGAGATGTGACT 966
Db 967 TCGAGAGCATTTGTGCA 982
Db 406 TTGAGAACACTGTGTGCA 421

RESULT 9

US-09-796-692-8936/c

Sequence 8936, Application US/09796692

Publication No. US20020198362A1

GENERAL INFORMATION:

APPLICANT: Gaiger, Alexander

APPLICANT: Algate, Paul A.

APPLICANT: Mannion, Jane

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THER

FILE REFERENCE: 2077_001200

CURRENT APPLICATION NUMBER: US/09/796,692

CURRENT FILING DATE: 2001-03-01

PRIOR APPLICATION NUMBER: 60/186,126

PRIOR FILING DATE: 2000-03-01

PRIOR APPLICATION NUMBER: 60/190,479

PRIOR FILING DATE: 2000-03-17

PRIOR APPLICATION NUMBER: 60/200,545

PRIOR FILING DATE: 2000-04-27

PRIOR APPLICATION NUMBER: 60/200,303

PRIOR FILING DATE: 2000-04-28

PRIOR APPLICATION NUMBER: 60/200,779

PRIOR FILING DATE: 2000-04-28

PRIOR APPLICATION NUMBER: 60/200,999

PRIOR FILING DATE: 2000-05-01

PRIOR APPLICATION NUMBER: 60/202,084

PRIOR FILING DATE: 2000-05-04

PRIOR APPLICATION NUMBER: 60/206,201

PRIOR FILING DATE: 2000-05-22

PRIOR APPLICATION NUMBER: 60/218,950

PRIOR FILING DATE: 2000-07-14

PRIOR APPLICATION NUMBER: 60/222,903

PRIOR FILING DATE: 2000-08-03

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; PRIOR APPLICATION NUMBER: 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,378
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 9597
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 8936
; LENGTH: 487
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-796-692-8936

Query Match      15.3%  Score 287; DB 9; Length 487;
Best Local Similarity 77.6%; Pred. No. 7e-58;
Matches 392; Conservative 0; Mismatches 95; Indels 18; Gaps 3;

QY 923 CGACTCTTCATCCTTTTGGAGTCAATCAAGCAAGATGTGACTTGAAGACATTGTGA 982
    ||||| ||||| ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 487 CGACTCTTCATCCTTCCTGGAATCATCAAGCAAGGTTGAGTTGAAACACTGTGCA 428
    983 CAAGTGATCTCCATCAGACAGAGCCCTGCGCTTCCACTGTGCTGACCCCATCT 1042
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 427 CAAGTGATCTTCATCAGCAGAGCCCTGACTTTCTTCCACTGTGCTGACCCCATCT 368
    1043 CTATGCTTCTCGCGGCGCAAGTTCAAAAGCTCTGCCAGCATGCACTCACTCCATGAG 1102
    ||||| ||||| ||| ||| ||| ||||| ||||| ||||| ||||| ||||| |||||
DB 367 CTATGCTTCTCGTGAGCCAAATTTAAACCTCTGCCAGCAGCAGCTCAGCTGTGAG 308
    QY 1103 CAGAGGCTCCAGCTCAAAATCTTTCCAAAGAAAGCGGGGTGACACTCTTCGCTTC 1162
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DB 307 CAGAGGCTCCAGCTCAAAATCTTTCCAAAGAAAGCGGGGTGACACTCTTCGCTTC 248
    QY 1163 CAGGAGTCAGATCCTCCAGTTTCCAGCCAGCTCAACCTTATGCAAGACTATATATA 1222
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DB 247 CACTGAGTCTGAGCTTTCAGATTTCACCTCAAGCTAA-----CACAGATGTAAAGA 196
    QY 1223 TATATATATATATATGATAAAGAACTTTTATGTACACATTTTCCAGATATAGAGAC 1282
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    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 135 TGACCAATATTTGACAGTTTATATGCTTGTGATTTTGT-----CTTGCTTTCT 82
    QY 1343 TAGTTTGTGAGGTTTGACTTAATTTATATATAATTTGTTTGTGTTTCATGTGA 1402
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DB 81 TAGTTTGTGAGTTTAAATGACTTATTTATA-----TAAATTTTGTGTTTCATTTG 26
    QY 1403 ATGAGCGTCTAGGACAGACCTGTGG 1427
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DB 25 ATGTGTGTCTAGGACAGACCTGTGG 1
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RESULT 10
US-10-040-862-8936/c
; Sequence 8936, Application US/10040862
; Publication No. US20030078396A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-01352005
; CURRENT APPLICATION NUMBER: US/10/040,862
; PRIOR APPLICATION NUMBER: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
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; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/223,378
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 09/796,692
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 8936
; LENGTH: 487
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-040-862-8936

Query Match      15.3%  Score 287; DB 9; Length 487;
Best Local Similarity 77.6%; Pred. No. 7e-58;
Matches 392; Conservative 0; Mismatches 95; Indels 18; Gaps 3;

QY 923 CGACTCTTCATCCTTTTGGAGTCAATCAAGCAAGATGTGACTTGAAGACATTGTGA 982
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DB 487 CGACTCTTCATCCTTCCTGGAATCATCAAGCAAGGTTGAGTTGAAACACTGTGCA 428
    983 CAAGTGATCTCCATCAGACAGAGCCCTGCGCTTCCACTGTGCTGACCCCATCT 1042
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 427 CAAGTGATCTTCATCAGCAGAGCCCTGACTTTCTTCCACTGTGCTGACCCCATCT 368
    QY 1103 CAGAGGCTCCAGCTCAAAATCTTTCCAAAGAAAGCGGGGTGACACTCTTCGCTTC 1162
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 307 CAGAGGCTCCAGCTCAAAATCTTTCCAAAGAAAGCGGGGTGACACTCTTCGCTTC 248
    QY 1043 CTATGCTTCTCGCGGCGCAAGTTCAAAAGCTCTGCCAGCATGCACTCACTCCATGAG 1102
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DB 367 CTATGCTTCTCGTGAGCCAAATTTAAACCTCTGCCAGCAGCAGCTCAGCTGTGAG 308
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DB 81 TAGTTTGTGAGTTTAAATGACTTATTTATA-----TAAATTTTGTGTTTCATTTG 26
    QY 1403 ATGAGCGTCTAGGACAGACCTGTGG 1427
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RESULT 11
US-10-251-385-65
; Sequence 65, Application US/10251385
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? Publication No. US20030105292A1
? GENERAL INFORMATION:
? APPLICANT: Behan, Dominic P.
? APPLICANT: Chalmers, Derek T.
? APPLICANT: Liaw, Chen W.
? TITLE OF INVENTION: No. US20030105292A1- Endogenous, Constitutively Activated Human G
? TITLE OF INVENTION: Protein-coupled
? TITLE OF INVENTION: Receptors
? FILE REFERENCE: AREN-0040
? CURRENT APPLICATION NUMBER: US/10/251,385
? CURRENT FILING DATE: 2002-09-20
? PRIOR APPLICATION NUMBER: US/09/170,496
? PRIOR FILING DATE: 1998-10-13
? NUMBER OF SEQ ID NOS: 294
? SOFTWARE: PatentIn version 3.1
? SEQ ID NO 65
? LENGTH: 1119
? TYPE: DNA
? ORGANISM: Homo sapiens
? 10-251-385-65

Query Match          10.6% Score 198.4; DB 9; Length 1119;
Best Local Similarity 53.8%; Pred. No. 1.1e-36;
Matches 456; Conservative 0; Mismatches 386; Indels 6; Gaps 2;
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205 AACGCTGCTGCTGCTGATCTCGAGAGCGGACCGGACAGACAGCATTCAGGAGAG 264
351 TACGGGCTGACCTGCTGATGAGTGCCTCTTGTGATCATCATCTCCCTTCTGGGA 410
265 TTCTCTTCCACCTGCGCGCGGCGGACCTGCTGCTTCTTCTTCTGCGCGT 324
411 GTTGATGCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 470
325 GCGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 384
471 TACATGTCACCTTACAGACAGCGCTTCTGATCTGCTGCTGCTGCTGCTGCTGCT 530
385 CACAAGTCAACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 444
531 CTGGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 590
445 CTGGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 504
591 GTCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 650
505 ACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 564
651 GACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 710
565 AAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 624
711 C---CGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 767
625 CAAGCAGAAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 684
768 CTGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 827
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828 AA---GGCGCAGCAGAGCGGCGGCTGAGAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 884
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885 TTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 944
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945 GTCAATCAAGCAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1004  
865 GCCGTGAGCAATACCTGCAAGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 924  
1005 GCCGTGCGCTTCTTCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1064  
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1065 TTCAAAAG 1072  
985 TTCCGCGAG 992
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RESULT 12
US-09-104-063-5
Sequence 5; Application US/09104063
Patent No. US20020168356A1
GENERAL INFORMATION:
APPLICANT: Lee, James
APPLICANT: Wood, William I.
TITLE OF INVENTION: PD4A Receptors
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/104,063
FILING DATE: 24-June-1998
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/701265
FILING DATE: 22-AUG-1996
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/664228
FILING DATE: 06-JUN-1996
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/076093
FILING DATE: 11-JUN-1993
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/810782
FILING DATE: 19-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P0706p2c2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1679 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear

US-09-104-063-5

Query Match 10.6% Score 198.4; DB 9; Length 1679;
Best Local Similarity 53.8%; Pred. No. 1.4e-36;
Matches 456; Conservative 0; Mismatches 386; Indels 6; Gaps 2;

231 TTCAATAGATCTTCCGCGCACCATCTTATCATCTTCTTGAAGGAGTGGG 290
513 TTCAAGGCGGTGTTCTGCGCCGCGGCTTACAGCTTATCTTCTGCGGCGATCGG 572

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 12, 2003, 13:44:23 ; Search time 305 Seconds
(without alignments)
13859.019 Million cell updates/sec

Title: US-09-367-052-1

Perfect score: 1877

Sequence: 1 ccatcctaatacagactcact.....aaaaaaaaaaaaaaaaaaaaa 1877

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1875.4	99.9	1877	19	AAV46370
2	1758	93.7	1758	20	AAZ27611
3	974.4	51.9	1737	16	AAO80521
4	974.4	51.9	1737	16	AAO99007
5	969.6	51.7	1737	13	AAO29506
6	952.8	50.8	1679	22	AAI65467
7	952.8	50.8	1679	22	AAI65467
8	951.8	50.7	1664	21	AAI61656
9	951.8	50.7	1664	21	AAZ40014

10	944.8	50.3	1670	24	ABK83803	Human CDNA differe
11	944.8	50.3	1670	24	ABN95645	Gene #2143 used to
12	939.8	50.1	1944	20	AAV15882	CDNA encoding G-pr
13	936.8	49.9	1588	20	AAZ27610	Human CXCR4 coding
14	934	49.8	5161	21	AAAF20896	Human CCR-4 CC che
15	934	49.8	5161	21	AAA34774	Human adenosine re
16	934	49.8	5161	24	AAH995951	CXCR4 gene. Homo
17	834.6	44.5	1317	19	AAV18357	Human RM3 seven tr
18	834.6	44.5	1317	24	AAH54255	Human 7TM receptor
19	834.6	44.5	1317	24	ABK54255	Human 7TM receptor
20	833	44.4	1317	15	AAQ66179	Seven transmembran
21	809.6	43.1	1059	21	AAZ38553	Human CX-C-chemok
22	809.6	43.1	1059	24	AAH99952	CXCR4 encoding seq
23	804.8	42.9	1059	23	AB197982	Non-endogenous hum
24	739.6	39.4	1119	24	AAK98241	Human cysteine-x-c
25	410.4	21.9	606	24	ABA92962	Human CDNA clone D
26	282	15.0	440	21	AAAC01917	Human secreted pro
27	203.2	10.8	611	20	AAV15883	CDNA encoding a pa
28	198.4	10.6	1119	21	AAA30626	Human G-protein-co
29	198.4	10.6	1679	13	AAO37107	New platelet facto
30	198.4	10.6	1679	16	AAO99009	Chemokine superfam
31	198.4	10.6	1679	16	AAQ80522	Human lymphocyte p
32	198.4	10.6	2818	20	AAV87710	Human Burkitt's ly
33	198.4	10.6	3620	22	ABA09117	Human Burkitt lymph
34	196.8	10.5	1119	21	AAA30727	DNA encoding human
35	195.8	10.4	2072	24	AAV17156	Mouse lymphoid spe
36	195.8	10.4	2084	24	AAK54274	Mouse 7 transmembr
37	195.8	10.4	2085	21	AAV91745	7TM receptor DNA s
38	193.8	10.3	1107	21	AAA30593	Human G-protein-co
39	193.8	10.3	1670	19	AAV26557	Human IP-10/Mig re
40	193.8	10.3	1670	24	ABN97338	Gene #3836 used to
41	193	10.3	1877	22	AAH35033	Human colon cancer
42	192.2	10.2	1107	21	AAA30714	DNA encoding human
43	192.2	10.2	1159	20	AAZ32713	Human chemokine re
44	192.2	10.2	1876	18	AAV72800	Human G-protein ch
45	189	10.1	4017	23	AAV83768	DNA encoding novel

ALIGNMENTS

RESULT 1	AAV46370	standard: CDNA to mRNA: 1877 BP.
ID	AAV46370;	
AC	AAV46370;	
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DT	20-NOV-1998 (first entry)	
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DE	Nucleic acid encoding a murine CXC chemokine receptor.	
XX		
KW	Mouse; CXC chemokine receptor; pre-B cell line DW34;	
KW	CXC chemokine pre-B cell stimulatory factor PBSP/SDF-1;	
KW	HIV infection; screening; inhibitor; AIDS; ds.	
XX		
OS	Mus sp.	
XX		
EH	Key	Location/Qualifiers
FT	CDS	120..1199
FT		/*tag= a
XX		
PN	MO9835035-A1.	
XX		
PD	13-AUG-1998.	
XX		
PF	07-FEB-1997;	97WO-JP00299.
XX		
PR	07-FEB-1997;	97WO-JP00299.
XX		
PA	(SHTO) SHTONOGI & CO LTD.	
XX		
PI	Iizasa H, Kishimoto T, Nagasawa T, Nakajima T, Tachibana K;	
PI	Yoshida N, Yoshie O;	

XX MPI: 1998-447232/38.
DR P-PSDB: AAW64778.
XX
PT Mouse CXK chemokine receptor binding to PBSF/SDF-1 pre-B cell
stimulatory factor - is useful for screening of potential HIV
infection and AIDS inhibitors
XX
PS Claim 3: Pages 39-42: 76pp: Japanese.
XX
CC The present sequence encodes a murine CXK chemokine receptor which
binds to the mouse CXK chemokine pre-B cell stimulatory factor
PBSF/SDF-1. The nucleic acid is isolated from mouse pre-B cell
line DM34. The receptor and cells expressing it can be used in the
study and mapping of the mechanism of HIV infection and in screening
of potential inhibitors of HIV infection and the development of AIDS.
XX
SQ Sequence 1877 BP: 469 A; 451 C; 406 G; 551 T; 0 other:

Query Match 99.9%; Score 1875.4; DB 19; Length 1877;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1876; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCATCTAATACGACTACTATAGGCTCGAGCGCCGCCGCGGAGGTGACAG 60
DB 1 CCATCTAATACGACTACTATAGGCTCGAGCGCCGCCGCGGAGGTGACAG 60
QY 61 TGACCCCTGAGGCGCTTTGGTCTCGGTACACCGCGGTGTAGAGGAGTTGGCA 120
DB 61 TGACCCCTGAGGCGCTTTGGTCTCGGTACACCGCGGTGTAGAGGAGTTGGCA 120
QY 121 TGGAACCGATCAGTGTAGTATATACACTTGTGTAATCTCTGAAGAAGTGGGCTTG 180
DB 121 TGGAACCGATCAGTGTAGTATATACACTTGTGTAATCTCTGAAGAAGTGGGCTTG 180
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DB 421 TGGCTGACTGTCATTTGGGAAATTTTGTAAAGCTGTCATATCATCTACACGTGA 480
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QY 961 GGTGCTGAGAGCATGTTGTCACAGTGTGATCTCATCAAGAGCCCTCGCTCTTCC 1020
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DB 1021 ACTGTTGCTGAAACCCATCTATGCTTCTGCGGCGCAAGTTCAAAAGCTCTGCC 1080
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QY 1141 GGGGTGAGACACTTCCGTCCTCAGGAGTCAAGATCCGATTTTTCACCTCAGCTAAC 1200
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QY 1201 CCTATGCAAAAGCTTATATATATATATATATATATATATATATATATATATAT 1260
DB 1201 CCTATGCAAAAGCTTATATATATATATATATATATATATATATATATATATAT 1260
QY 1261 ACATTTTCCAGTATATAGAGACTGACAGCTCTGTGACGTTTTTTTTTTTAAATGA 1320
DB 1261 ACATTTTCCAGTATATAGAGACTGACAGCTCTGTGACGTTTTTTTTTTTAAATGA 1320
QY 1321 CTGTTGGAGTTATGTTCTCTAGTTTGTGAGAGTTGACTTAAATATATATAT 1380
DB 1321 CTGTTGGAGTTATGTTCTCTAGTTTGTGAGAGTTGACTTAAATATATATATAT 1380
QY 1381 GTTTTTTGTGTTTCAATGTAATGAGCTGTAGAGAGCTGTGGCCAACTTTTAAT 1440
DB 1381 GTTTTTTGTGTTTCAATGTAATGAGCTGTAGAGAGCTGTGGCCAACTTTTAAT 1440
QY 1441 AGCTGTTATCTGTGTAGAGCTGTAGAGCTGTAGAGAGCTGTAGAGAGCTGTAGAG 1500
DB 1441 AGCTGTTATCTGTGTAGAGCTGTAGAGCTGTAGAGAGCTGTAGAGAGCTGTAGAG 1500
QY 1501 TGTGTGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAAT 1560
DB 1501 TGTGTGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAAT 1560
QY 1561 TTTCCAGAGAGCAGCCACCCACCCACCCACCCACCCACCCACCTTAAATGTTGGTAT 1620
DB 1561 TTTCCAGAGAGCAGCCACCCACCCACCCACCCACCCACCCACCTTAAATGTTGGTAT 1620
QY 1621 GCTGTGTAATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1680
DB 1621 GCTGTGTAATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1680
QY 1681 AGATGACATTTAAACCAAGCTTAAATGTTGTTGTTGTTGTTGTTGTTGTTGTT 1740
DB 1681 AGATGACATTTAAACCAAGCTTAAATGTTGTTGTTGTTGTTGTTGTTGTTGTT 1740
QY 1741 GTTTGTTTTCAGTTTCAAGAGTATGATGATGATGATGATGATGATGATGATGATG 1800
DB 1741 GTTTGTTTTCAGTTTCAAGAGTATGATGATGATGATGATGATGATGATGATGATG 1800
QY 1801 TATTACATTTGTTTAAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTA 1860
DB 1801 TATTACATTTGTTTAAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTA 1860

Qy	1861	AAAAAAAAAAAAAAAA	1877
Db	1861	AAAAAAAAAAAAAAAA	1877

RESULT 2	
AAZ27611	
ID	AAZ27611 standard; DNA; 1758 BP.

AC AAZ27611;

DT 16-DEC-1999 (first entry)
XX

DE Mouse CXCR4 coding sequence.

KM CXCR4; mouse; neovascularisation; inhibitor; solid cancer; therapy;
KM tissue repairing agent; vascularisation; ss.

Mus sp.

W09948528-A1.

PD 30-SEP-1999

PF 23-MAR-1999; 99WO-JP01448.

PR 24-MAR-1998; 98JP-0095448.

PA (CHUS) CHUGAI SEIYAKU KK.
PA (CHUS) CHUGAI SEIYAKU KK.

XX
XX
DT

XX
DB WBT: 1000-501043/EO

DR P-PSDB; AAY39994.
XX

PT	Vascularisation
XY	

PS Disclosure; page 50-51; 63pp; Japanese
xy

CC This sequence encodes the mouse CXCR4

CC remedies for diseases pathologically caused by neovascularisation and
CC tissue repairing agents containing as the active ingredient a substance
CC capable of potentiating CXCR4, based on a finding that vascularisation
CC inhibited in a CXCR4 knockout mouse, it becomes possible to prepare

50 Sequence 1758 BP; 447 A; 414 C; 369 G; 528 T; 0 other;

Query Match	93.7%	Score 1758	DB 20	Length 1758
Best Local Similarity	100.0%	Pred. No. 0		
Matches 1/58; Conservative	0	Mismatches	0	Gaps 0

QY 120 TTGGAAACCGATCAGTGTAGTATATACACTTGTAAATACTCTGAAACAAAGGGGGTCT 179

Db 1 ATGGAAACCGATCAGTGTAGTATATACACTTGTAAATACTCTGAAACAAAGGGGGTCT 60

QY 180 GGAGACTATGACTCCACAGAGAACCTTCTCCGGATGAAAAACGTCATTTCATATAG 239

Db 61 GGAGACTATGACTCCACAGAGAACCTTCTCCGGATGAAAAACGTCATTTCATATAG 120

QY 240 ATCTTCCTGCCCAACCATCTACTTCATCATCTTCTTGACGGCATACTCGGCAATGATG 299

Db 121 ATCTTCCTGCCCAACCATCTACTTCATCATCTTCTTGACGGCATACTCGGCAATGATG 180

QY 300 GTGATCTCTGTCATGGGTTTACCAGAGAAGACTTAAAGAGCATGACGACAAGTACCGGGCTG 359

[illegible]

Dd		1261	TGTTTTTTTGGTTTTCATGTGAATGAGCGCTTAGCAGACCTGTGGCCAAAGTTCTTAG	1320
Oy		1440	TAGCTGTTTATCTGTGTGTAGACTGTAGAACCTGTAGAGGAAGAACTGAACATTCCAGA	1499
Dd		1321	TAGCTGTTTATCTGTGTGTAGACTGTAGAACCTGTAGAGGAAGAACTGAACATTCCAGA	1380
Oy		1500	ATGTGTGTTAATTGAATAAAGCTAGCCGTGATCCTCAGCTGTGTGCATTAATCTCTTC	1559
Dd		1381	ATGTGTGTAAATTGAATAAAGCTAGCCGTGATCCTCAGCTGTGTGCATTAATCTCTTC	1440
Oy		1560	ATTCGAGAGACACCACCCCAACCCCAACCCCAACCCCAACCCCAATTTAAATTGTGGTTA	1619
Dd		1441	ATTCGAGAGACACCACCCCAACCCCAACCCCAACCCCAACCCCAATTTAAATTGTGGTTA	1500
Oy		1620	TGCTGTGTGATGTTTGTAA	1679
Dd		1501	TGCTGTGTGATGTTTGTAA	1560
Oy		1680	AAGATGGACATTAACAACCAAGCCGTGAATGCTGTGTAATGCTGGGGTTTTTTTCTT	1739
Oy		1561	AAGATGGACATTAACAACCAAGCCGTGAATGCTGTGTAATGCTGGGGTTTTTTTCTT	1620
Dd		1740	TGTTTGTTTTTTCAGTTTCAAGAGTAGATGATTCAGTCCCTACAAATGTACAGTCTT	1799
Oy		1621	TGTTTGTTTTTTCAGTTTCAAGAGTAGATGATTCAGTCCCTACAAATGTACAGTCTT	1680
Dd		1800	GTAATTACATTTGTAATAAAGCTCATGATGTAATACTTAATAAAAAAAAAAAAAAAA	1859
Oy		1681	GTAATTACATTTGTAATAAAGCTCATGATGTAATACTTAATAAAAAAAAAAAAAAAA	1740
Oy		1860	AAAAAAAAAAAAAAAAAAAA 1877	
Dd		1741	AAAAAAAAAAAAAAAAAAAA 1758	
 RESULT 3 AAQ80521 ID AAQ80521 standard; cDNA: 1737 BP.				
xx		AAQ80521;		
ac		18-JUL-1995 (first entry)		
xx		Human monocyte PF4AR cDNA.		
de		Interleukin-8 receptor; IL-8 receptor; PF4AR;		
xx		platelet factor superfamily receptor; monocytic; chemotactic;		
Kw		inflammation; inflammatory disease; arthritis; emphysema; cystic;		
Kt		fibrosis; colitis; bronchitis; meningitis; therapeutic; ss.		
OS		Homo sapiens.		
xx		Key	Location/Qualifiers	
FH		CDS	91..1149	
Tt		/+tag= a		
xx		W09428931-A.		
PN		22-DEC-1994.		
PD		07-JUN-1994;	94WO-US06380.	
PE		11-JUN-1993;	93US-U0076093.	
PR				
xx		(GENE) GENENTECH INC.		
PA		Chuncharapai A, Hebert C, Kim KJ, Lee J;		
xx		WPI; 1995-036114/05.		
DR		P-PSDB; AAR68812.		
xx		Treatment of inflammatory disorders - by administering an		
PT		antibody capable of binding a platelet factor 4 superfamily		

Query Match	Best Local Similarity	Score	DB	Length
Matches 1391: Conservative	76.1%	974.4	16	1737
		1.9e-174		
		Mismatches 301: Indels 136: Gaps 10		
50	CGAGTACGACGACCCCTGTGAGGGGGTGGGCTCCGGTACCCACCACCGCTGTAGAC	109		
20	GGCGGGCCCAAGATGACCGCGGAGGCGCTGAGTGCTCCATACCCACCGATGGAGAC	79		
110	GAGTGTGGCATGAGAACCGATCAGTGTGATATACATCTTGATTAACCTACTGAGA	169		
80	CAGCGGTATACCATGGA-----GGGATCAGTATATACACTTAGATTAACACCGAGA	134		
170	AGTGGGGTCTGGAGACTATGACTCCAAAGAACCCGCTCCGGAGTAAAGCTCA	229		
135	AATGGGCTCAGGGGACTATGACTCATGAAAGAACCCCTGTTCCGGAGAAATGCTAA	194		
230	TTTCATATGAGATCTTCCTGCTCCACCATCTACTTCATCTTCTTGACCTGCGATAGT	289		
195	TTTCATATAAATCTTCCTGCTCCACCATCTACTTCATCTTCTTAAACGGGATTTGG	254		
290	CAATGATATGGGATCTGCTGTCATGGGTATCCAGAGAAGAGTAAAGAGCATGACGACA	349		
255	CAATGATATGGGATCTGCTGTCATGGGTATCCAGAGAAGAGTAAAGAGCATGACGACA	314		
350	GTACGGGTGCACCTGTGAGTGGCTGACCTCTTGTGATACACCTCCCTTGAGG	409		
315	GTACAGGCTGCACCTGTGAGTGGCTGACCTCTTGTGATACACCTCCCTTGAGG	374		
410	AGTTATGCTCAGCTGTGACTGCTACTCTTGGGAATTTTGTGTAGGCTGCTCATATCAT	469		
375	AGTTATGCTCAGCTGTGACTGCTACTCTTGGGAATTTTGTGTAGGCTGCTCATATCAT	434		
470	CTACACTGTCAACCTCTACAGAGCGCTTCTCATCTGCGCTTCATACAGCCTGACCGTA	529		
435	CTACACTGTCAACCTCTACAGAGCGCTTCTCATCTGCGCTTCATACAGCCTGACCGTA	494		
530	CCTCGCATTTGTCAAGCGCCACCAACAGTCAAAAGGCGCAAGAACTGCTGGTGAAGGC	589		
495	CCTCGCATTTGTCAAGCGCCACCAACAGTCAAAAGGCGCAAGAACTGCTGGTGAAGGC	554		
530	AGTCTATGTGGGCTGTGATCCAGCCCTCTCTGACTATACCTGACTTATCTTTCG	649		
555	GGTCTATGTGGGCTGTGATCCAGCCCTCTCTGACTATACCTGACTTATCTTTCG	614		
650	CGAGTTCAGCCAGGGGAGCATCAGTCAGGGGGATGACAGGTACATCTGTGACCGCTTAA	709		
615	CACG-----TCAGTGAAGGACATGACATGATATCTGTGACCGCTTAA	659		
710	CCCCGATAGCCTGTGATGTGTGTTTCAATTCAGCATATATATATGAGGCTGCTACTCT	769		
660	CCCCGATAGCCTGTGATGTGTGTTTCAATTCAGCATATATATATGAGGCTGCTACTCT	719		
770	GCCGGCATCGTATCTCTCTGTTACTGATCATCTCTAAGTGTCAACTCCAA	829		
720	GCCTGTATTTGATCATCTCTCTCTGTTACTGATCATCTCTAAGTGTCAACTCCAA	779		
830	GGGGCACCAGAAAGGCGCAAGGCGCTTCAAGACCAACATGATCTCTGCTTCTTCCG	889		
780	GGGGCACCAGAAAGGCGCAAGGCGCTTCAAGACCAACATGATCTCTGCTTCTTCCG	839		

RESULT 4
AAQ99007
ID
AAQ99007 strand; cdNA; 1737 BP.

AA	QAQ99007;
XX	
DT	26-MAR-1996 (first entry)
XX	
DE	Chemokine superfamily receptor coding sequence.
XX	
KW	Interleukin; IL-8; inflammation; psoriasis; dermatitis;
KM	rheumatoid arthritis; inflammatory bowel disease;
KW	chronic lung inflammation; treatment; antibody;
KM	affinity purification; detection; ss.
XX	
OS	Homo sapiens.
XX	
PN	US5440021-A.
XX	
PD	08-AUG-1995.
XX	
PF	29-MAR-1991; 91US-0677211.
XX	
PR	25-FEB-1994; 94US-0202056.
PR	29-MAR-1991; 91US-0677211.
XX	
PA	(CHUN/) CHUNTHARAAPAI A. (HEBE/) HEBERT C. (KIMR/) KIM R J. (LEEJ/) LEE J.
PI	Chuntharapai A, Hebert C, Kim RJ, Lee J; WI: 1995-283151/37. P-PDSB: MAR80757.
PT	New antibodies against interleukin 8 type B receptor - used to treat or prevent inflammation, also for detecting receptor expression and purification.
PX	
PS	Example 2; Columns 47-50; 62pp; English.
XX	
CC	Antibodies directed against the interleukin-8 receptor B can be used to treat or prevent inflammation e.g. psoriasis, dermatitis, rheumatoid arthritis and particularly inflammatory bowel disease and chronic lung inflammation. When immobilised, these antibodies may be used to detect Interleukin-8 receptor B expression in cells and tissues and for affinity purification of interleukin-8 receptor B from cells. This sequence is an additional chemokine superfamily receptor which was identified by probing lambda libraries of genomic DNA from a human monocytic-like cell line (U-60) and human peripheral blood lymphocytes using a large fragment of the interleukin-8 type A receptor DNA (see AAQ99006).
XX	
SQ	Sequence 1737 BP; 454 A; 411 C; 373 G; 499 T; 0 other; Query Match 51.9%; Score 974.4; DB 16; Length 1737; Best Local Similarity 76.1%; Pred. NO.1.9e-174; Matches 1391; Conservative 0; Mismatches 301; Indels 136; Gaps 10
OY	50 GCAGGTACGACTGACCCTCTGAAGCGTTGGTGTCCGGTAACAACACGCTGTAGAC 109 DB 20 GGCGGGGCCCAAGAATGCAGCAGGCGCCGAGTGCTCCAGTAGCCACCGCATCTGGAGAAC 79 OY 110 GAGTGTTCATTGGAACCGATCAGTGAGTAATAACACTTGTGATTAAGTACTCTGAGA 169 DB 80 CAGCGGTTACCATGGA-----GGGATATAGTATATACACTTGAAGTAACCGAGAGA 134 OY 170 AGTGGGGTCTGAGACTATGACTCCACAAAGAACCCCTCTCGGGATGAAAACGTCCA 229 DB 135 AATGGCGCTCAGGGGACTATGACTCATGAGAAGAACCCCTGTTCCGTGAAGAAATGCPNA 194 OY 230 TTTCATATGAGATCTTCGCCCCACCATCTACTTCAATCAATCTTCTGAGCTGAGATAGTGG 289 DB 195 TTTCATATTAATCTTCTGCCCCACCATCTACTTCAATCTTCTTAACGTGGCATTTGTGG 254 OY 290 CAATGATTTGGTGAATCGTATCGTATCGGTATACAGAGAAGACGTAAGACATCACCGACAN 349

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Db      ||||| 255 CAATGATTTGGTATCTGTCATGGGTTACCAAGAAACTGAGAGCATGACGAGACA 314
Qy      350 GACACGGGCTGCACCTGTGACGTGGCTGACCTCTTTTGTGATCAGACTCCCTTCTGGGC 409
Db      315 GATACAGGGGTCACCTGTGACGTGGGCGACCTCTTTTGTGATCAGACTCCCTTCTGGGC 374
Qy      410 ACTTATGTCATGCTGACGTGACGTGGGAAATTTTGTGTAAGGCTGTCCATATCAT 469
Db      375 ACTTATGTCATGCTGACGTGACGTGGGAAATTTTGTGTAAGGCTGTCCATATCAT 434
Qy      470 GTACACTGTCAACCTCTACAGCAGCGCTTCATCTGGCTTCATCAGCTTGACCGGTA 529
Db      435 GTACACAGTCAACCTCTACAGCAGCGCTTCATCTGGCTTCATCAGCTTGACCGGTA 494
Qy      530 CCTGGCATTTGTCACGCGCCACACAGTCAAGGCCAAGAACTGCTGGCGTAAGAGC 589
Db      495 CCTGGCATTTGTCACGCGCCACACAGTCAAGGCCAAGAACTGCTGGCGTAAGAGC 554
Qy      590 ACTCTATGTGGGCTGTGATGCCAGCCCTCTCTGACTATACGTGACCTTCATCTTTC 649
Db      555 GGTCTATGTGGGCTGTGATGCCAGCCCTCTCTGACTATACGTGACCTTCATCTTTC 614
Qy      650 CGACGTCAAGCCAGGGGGACATGATCAGGGGATGACAGGTACATCTGTGACCGCTTTA 709
Db      615 CAACG-----TCAGTAGGACAGATGACAGATATATCTGTGACCGCTTTCTA 659
Qy      710 CCCCGATGCTGTGATGCTGTGTTTCAATTCAGCATATTAAGTGGTGTCTATCT 769
Db      660 CCCCGATGCTGTGATGCTGTGTTTCAATTCAGCATATTAAGTGGTGTCTATCT 719
Qy      770 GCCCGCATGCTGTGATGCTGTGTTTCAATTCAGCATATTAAGTGGTGTCTATCT 829
Db      720 GCCCGATGCTGTGATGCTGTGTTTCAATTCAGCATATTAAGTGGTGTCTATCT 779
Qy      830 GGGCCACCAAGAGCCGACAGGCGCTCAAGACAGTCACTCTATCTTCTTTC 889
Db      780 GGGCCACCAAGAGCCGACAGGCGCTCAAGACAGTCACTCTATCTTCTTTC 839
Qy      890 CTGCTGGCTGCTATTTATGTTGGGATGATGATGATGATGATGATGATGATGAT 949
Db      840 CTGCTGGCTGCTATTTATGTTGGGATGATGATGATGATGATGATGATGATGAT 899
Qy      950 CAGCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1009
Db      900 CAGCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 959
Qy      1010 GCGCTTCTTCCACTGTGCTGACACCCCTCTATGCTTCTGCGGCGCAAGTTC 1069
Db      960 ACCTTCTTCCACTGTGCTGACACCCCTCTATGCTTCTGCGGCGCAAGTTC 1019
Qy      1070 AAGCTGTGCGGACATGACATGACATGACATGACATGACATGACATGACATGACAT 1129
Db      1020 AAGCTGTGCGGACATGACATGACATGACATGACATGACATGACATGACATGACAT 1079
Qy      1130 CAAAGGAAAGCGGGGTGACACTCTTCGCTCCACGAGTACAGATCTCCAGTTTCA 1189
Db      1080 CAAAGGAAAGCGGGGTGACACTCTTCGCTCCACGAGTACAGATCTCCAGTTTCA 1139
Qy      1190 CTCGAGCTTACCTTATGCAAGACTTATATATATATATATATATATATATATAT 1249
Db      1140 CTCGAGCTTACCTTATGCAAGACTTATATATATATATATATATATATATATAT 1191
Qy      1250 TTTTATGTTACATTTTCCAGATTAAGAGACTGACGCTGTGACAGTTTCTTTT 1309
Db      1192 TTTTATGTTACATTTTCCAGATTAAGAGACTGACGCTGTGACAGTTTCTTTT 1251
Qy      1310 TTTTATGTTACATTTTCCAGATTAAGAGACTGACGCTGTGACAGTTTCTTTT 1369
Db      1252 TTTTATGTTACATTTTCCAGATTAAGAGACTGACGCTGTGACAGTTTCTTTT 1305
Qy      1370 ATATATAATTTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGT 1429

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Db      1306 TTTATA-----TAATTTTTTTTGTTCATATGATGTGTGTGACGAGACCTGTGGC 1361
Qy      1430 AAGTCTTAGTACGCTGTTTATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1489
Db      1362 AAGTCTTAGTACGCTGTTTATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1413
Qy      1490 ACATTTCCAGAAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1549
Db      1414 ACATTTCCAGAAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1473
Qy      1550 TAATCTTTCATTTCCAGAGACACCCACCCACCCACCCACCCACCCACCTTTAAT 1609
Db      1474 TAGATTAATCTTCTCA----- 1488
Qy      1610 TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1669
Db      1489 -----TTCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1525
Qy      1670 TTTTCTGTAAGAGATGACCTTAAACCAAGCCGTAAGTGTGTGTGTGTGTGTGTGTGT 1729
Db      1526 TTTGCTGTAGAGATGACCTTATACCAAGCCCAAGTGTGTGTGTGTGTGTGTGTGT 1581
Qy      1730 TTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1789
Db      1582 -----TTTTCACTTTTCAAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1623
Qy      1790 GTACAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1849
Db      1624 GTACAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1683
Qy      1850 AAAAAAAAAAAAAAAAAAAAAAAAAA 1877
Db      1684 AAAAAAAAAAAAAAAAAAAAAAAAAA 1711

RESULT 5
AAQ29506
ID AAQ29506 standard; DNA; 1737 BP.
XX
AC AAQ29506;
XX
DT 12-MAR-1993 (first entry)
XX
DE New platelet factor 4 receptor superfamily member PF4ARI.
XX
IL-8R; G-protein coupled receptor family: rhodopsin superfamily;
XX
KW pro-inflammatory cytokine; 8r.20.15; ss.
XX
OS Homo sapiens.
XX
FH key Location/Qualifiers
FT CDS 91..149 /tag=a
FT FT /product= PF4ARI
FT FT
XX
PN WO9217497-A.
XX
PD 15-OCT-1992.
XX
PE 23-MAR-1992; 92MO-US02317.
XX
PR 29-MAR-1991; 91US-0677211.
PR 19-DEC-1991; 91US-0810782.
XX
PA (GETH ) GENENTECH INC.
XX
PI Holmes WE, Lee J, Wood WI;
XX
DR WPI: 1992-366191/44.
XX
DR P-PSDB: AAR27792.
XX
PT Isolated human platelet factor 4 super-family receptor
polypeptide and corresp. antibodies and DNA - useful as

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ID	AA165467	standard: DNA: 1679 BP.
XX	AA165467:	
XX	10-DEC-2001 (first entry)	
XX	Nucleotide sequence of a human polynucleotide.	
XX	Human; receptor; DC-SIGN; dendritic cell; T lymphocyte; HIV;	
XX	gp120; C-type lectin; ICAM3; HIV entry; T cell; macrophage;	
XX	HIV infection; ss.	
XX	Homo sapiens.	
XX	MO200164752-A2.	
XX	07-SEP-2001.	
XX	28-FEB-2001; 2001WO-US06322.	
XX	02-MAR-2000; 2000US-0517605.	
XX	(UYNY) UNIV NEW YORK STATE.	
XX	(UYNI-) UNIV NIJMEGEN.	
XX	Littman DR, Kwon D, Van Kooyk Y, Geljtenbeek T;	
XX	WPI; 2001-602565/68.	
XX	An antibody for the treatment or prevention of HIV-infection comprises	
XX	a gp120 portion which binds to DC-SIGN or is exposed upon gp120 binding	
XX	of DC-SIGN due to concomitant conformational change .	
XX	Disclosure; Page 126-127; 131pp; English.	
XX	The specification describes an antibody which is specific for an	
XX	antigenic fragment of gp120. This antigenic fragment binds to DC-SIGN	
XX	or is exposed upon gp120 binding of DC-SIGN due to concomitant	
XX	conformational change. DC-SIGN is a receptor that is specifically	
XX	expressed on dendritic cells and facilitates infection of T lymphocytes	
XX	with HIV. DC-SIGN is identical to a HIV-1 gp120-binding C-type lectin.	
XX	DC-SIGN binds ICAM-3 (which is expressed constitutively on T lymphocytes)	
XX	with high affinity. The antibody of the invention inhibits the trans	
XX	enhancement of HIV entry into a T cell or macrophage facilitated by	
XX	dendritic cells. The antibody is useful to treat or prevent HIV	
XX	infection. The present sequence represents a human polynucleotide,	
XX	which is used in the course of the invention.	
XX	Sequence 1679 BP; 407 A; 400 C; 368 G; 504 T; 0 other:	
XX	Query Match 50.8%; Score 952.8; DB 22; Length 1679;	
XX	Best Local Similarity 80.2%; Pred. No. 2,2e-170;	
XX	Matches 1210; Conservative 0; Mismatches 252; Indels 46; Gaps 6	
XX	44 GCAGGTGAGTAGTACAGTACCTCTGAGCGCTTTGGTCTCCGTAACACACCGCTG 103	
XX	12 GCGGAGAGAGTAGAAGTACGCGCGGCGCTAGTCCATCAACCGCATCG 71	
XX	104 TAGAGCGAGTGTGGCATGGAACCATGATGCTGATATATACACTTCGATATCTAC 163	
XX	72 GAGAACCGCGGTTCATGGA-----GGGATTCAGTATATACACTTCAGATATCTAC 126	
XX	164 TGAAGAACTGGGGTCTGAGACTATAGTCCCAACAGGAACCTCTCCGAGTAA 223	
XX	127 CGAGAAATGGGCTCAGGGACTATAGTCCATGAAGAACCTCTTCCGTAAGAA 186	
XX	224 CGTCATTTCAATAGATCTTCTGCCACACATCTACTTCAATCTCTTGACGCGAT 283	
XX	187 TGTAAATTTCAATAAATCTTCTCTCCACCATCTACTTCATCAATCTCTTAACGGCAT 246	
XX	284 AGTGGCAATGATGTGATCTGATCTGATGCTTATCCAGAAAGATTAAGAGCATGAC 343	

D	b	247	TGTGGCAATGATTTGGTCAATCCCTGGTGCATGSGTTACCAAGAAAGAACTGCAGAACATGATGAC	306
Q	y	344	GGACAAGTACCGCGGTGACACCTGTGACGTGGTGACCTCTCTTTGTCAATCAACATCCCTTT	403
D	b	307	GGACAAGTACAGCGCTGCACCTGTGACGTGGCGGACCTCTCTTTGTCAATCAACATCCCTTT	366
Q	y	404	CTGGGCAATGATGCCATGGCTGACCTGGTACTTTGGGAAATTTTGTGTAAAGCTGTGCCA	463
D	b	367	CTGGGCAATGATGCCCTGGTGCACCACTGGTACTTTGGGAAATTTTGTGTAAAGCTGTGCCA	426
Q	y	464	TATGATCTACACTGTCAACCTCTACAGACAGGTTCTCATCTCTGGCTTTCAATCAGCTTGA	523
D	b	427	TGTATCTACACAGTCAACCTCTACAGACAGTGTCTCATCTCTGGCTTTCAATCAGCTTGA	486
Q	y	524	CCGGTACCTCGCCATTGTCCACGGCCACCAACAGTCAAAAGGCCAAGAAACTGTGCTGA	583
D	b	487	CCGGTACCTCGCCATTGTCCACGGCCACCAACAGTCAAAAGGCCAAGAAACTGTGCTGA	546
Q	y	584	AAAGGCAATCTATGTGGCGCTGTGGATGCCAGCCCTCTCTGACTATACCTGACTTCAT	643
D	b	547	AAAGGCAATCTATGTGGCGCTGTGGATGCCAGCCCTCTCTGACTATACCTGACTTCAT	606
Q	y	644	CTTTGCGGAGTCAAGCCAGGGGAGCATCAGTCAAGGGAGTACAGAGTATCATCTGTGACG	703
D	b	607	CTTTGCGGAGTCAAGCCAGGGGAGCATCAGTCAAGGGAGTATCATCTGTGTGACG	651
Q	y	704	CCTTTACCCCGATAGCTGTGGATGATGGTGTTTCAATTCCAGCATATATGTGGGCT	763
D	b	652	CTTCTACCCCGATAGCTGTGGATGATGGTGTTTCAATTCCAGCATATATGTGGGCT	711
Q	y	764	CATCTCGCCCGGATCTGTATCTCTCTCTGTACTGATCATATCTCTTAAGCTGTACA	823
D	b	712	TATCTCGCCCGGATGTGTGTATCTCTCTCTGTACTGATCATATCTCTTAAGCTGTACA	771
Q	y	824	CTTCAAGGGCCACCAGAAAGCGCAAGGCCCTCAAGCAGTCAATCTCATCTAGCTTT	883
D	b	772	CTTCAAGGGCCACCAGAAAGCGCAAGGCCCTCAAGCAGTCAATCTCATCTAGCTTT	831
Q	y	884	CTTTGCGTGTGCTGCCATATATATGTGGGATCAGATCGATCTTCAATCCTTTTGGG	943
D	b	832	CTTTGCGTGTGCTGCCATATATATGTGGGATCAGATCGATCTTCAATCCTTTTGGG	891
Q	y	944	AGTATCAGCAAGAGATGTGACTTCCAGAGATTTGTGCACAAGTGGATCTCCATCACAGA	1003
D	b	892	AATCATCAAGCAAGAGGTGTGAGTTGAGAAACATGTGCACAAGTGGATTTCCATCACAGA	951
Q	y	1004	GGCCCTGCGCTCTTCCACATTTTCCAGAACCCCATCTCATGCTCTCCCTGGGGCCAA	1063
D	b	952	GGCCCTGCGCTCTTCCACATTTTCTGTGAACCCCATCTCATGCTCTTCCCTGGAGCCAA	1011
Q	y	1064	GTTCAAAAGCTCTGCCACAGATGCATCACTCATGCATGACGAGGCTCCACCTCAAGAT	1123
D	b	1012	ATTTAAAAACCTCTGCCACAGCACTACACTCTGTGACGAGAGGTTGCCACCTCAAGAT	1071
Q	y	1124	CCTTTCCAAAGGAAGGGGGTGGACACTCTTCCGTCTCCAGGAGTCAAGATCTCTCAG	1183
D	b	1072	CCCTTCCAAAGGAAGGAGGTGACATTCATCTGTTCCACTGACATGCTGCTTCAAG	1131
Q	y	1184	TTTTTCACCTCCAGTCAACCTTATGCAAAAGCTTATATATATATATATATATATATAT	1243
D	b	1132	TTTTTCACCTCCAGTCAACAGATGTAAAAAGCTTTT-----TTTATTCAGTAAATTA	1183
Q	y	1244	GAACCTTTTATATGTTACACATTTTTCAGATATAGAGAGCTGACCAAGTCTTGATACGTTT	1303
D	b	1184	ACTTTTATATGTTATACACATTTTTCAGATATATAGAGAGCTGACCAATATTTATACGTTT	1243
Q	y	1304	TTTTTTTTTTTAAATTTGACTGTGGGAGTTTATGTTCTCTATGTTTGTGTAGGTTTGACT	1363
D	b	1244	TATGCTGTGTTGGATTTTGT-----CTGTGTTTCTTATGTTTGTGTAGGTTTAAAT	1297
Q	y	1364	TAAATTAATTAATTAATGTTTTTTTGTGTTTCAATGTAAGAGAGCGTCTACGAGAGCT	1423
D	b	1298	GACTTATTTATA-----TAAATTTTTTTTGTGTTTCAATGTAAGAGTGTGTGTAGGAGAGCT	1353

Oy	1424	GTGGCCAAAGTCCTTAGTAGAGCGTTTACTGTGCTGTAGACGCTAGAACGTGTAGAGAGAGA	14683
Db	1354	GTGGCCAAAGTCCTTAGTAGAGCGTTTACTGTGCTGTAGACGCTAGAGAA-----AAGGG	14059
Oy	1484	AACAGCAATCCAGCATGCTGTGCTGAATTAATGAATAAGAGCTAGCCGTCATCCTCAGCTCTT	15433
Db	1406	AACAGCAATCCAGCAGCGGTGTATGTGAATCATCAGTAAGAGCTGAATATGATCCCAAGCTGT	14655
Oy	1544	GCTGCATTA 1551	
Db	1466	TATGCATTA 1473	
RESULT 7			
AD12801	AADI2801 standard; DNA; 1679 BP.		
AD12801;	16-OCT-2001 (first entry)		
DE	Human neuropeptide Y (NPY) Y3 receptor DNA.		
KW	Human; neuropeptide Y; NPY; bone disease; bone mass; gene therapy;		
KW	cerebrospinal fluid; CSF; inositol phosphate; IP; Paget's disease;		
KW	fracture; extracellular signal-regulated kinase; ERK; osteoporosis;		
KW	osteopenia; bone metastasis; neurotransmitter; osteogenic;		
KW	NPY Y3 receptor; ds.		
OS	Homo sapiens.		
FT	Key	location/Qualifiers	
FT	CDS	89..1147	
FT		/*tag= a	
FT		/product= "Human neuropeptide Y (NPY) Y3 receptor"	
PN	WO200153477-A1.		
PD	26-JUL-2001.		
PE	22-JAN-2001; 2001WO-US02040.		
PR	20-JAN-2000; 2000US-0489872.		
PA	(BAYU) BAYLOR COLLEGE MEDICINE.		
PA	(AMLI/) AMLING M.		
PA	Amling M, Karsenty G, Ducky P;		
DR	MPI: 2001-488709/53.		
DR	P-PSDB: AAE06690.		
PT	Treating or preventing reduced bone mass, e.g. osteoporosis, by		
PT	reducing the level of neuropeptide Y activity in blood or cerebrospinal		
PT	fluid -		
PS	Example 7; page 84-85; 102pp; English.		
XX	The present invention relates to a method for treatment or prevention of		
CC	bone diseases characterised by loss of bone mass, comprises administering		
CC	to a mammal a compound that lowers the level of neuropeptide Y (NPY) in		
CC	the serum or cerebrospinal fluid (CSF) or a compound that lowers the		
CC	level of inositol phosphate (IP) or extracellular signal-regulated kinase		
CC	(ERK). The method is specifically used to treat (including by gene		
CC	therapy) or prevent osteoporosis, osteopenia or Paget's disease, but may		
CC	also be used e.g., in cases of fractures or bone metastases. These		
CC	diseases may also be diagnosed by detecting elevated NPY levels.		
CC	clinical monitoring of treatment, assessing efficacy of compounds in		
CC	clinical trials and for identifying subjects at risk. The present		
CC	sequence is a human NPY Y3 receptor DNA.		
XX	Sequence 1679 BP; 407 A; 400 C; 368 G; 504 T; 0 other:		

Query Match	50.88:	Score 952.8:	DB 22:	Length 1679:
Best Local Similarity	80.28:	Pred. N.2.2e-170:		
Matches 1210:	Conservative 0:	Misatches 252:	Indels 46:	Gaps 6:
QY	44	GCAGGTCCAGGTACAGTGAACCTCTAAGGGTGTGGTCCCGGTAAACACACAGGCTG	103	
Db	12	GGCGCAGCAGGTACCAAAAGTGACGCCCGAGGCCCTGAGTGCCTCCAGTAGCCACCGCATCTG	71	
QY	104	TAGAGCAGTGTGGCCATGGAACCGATCAGTGTGATATATACCTTCTGTAACTACTC	163	
Db	72	GAGAACCAAGCGGTACCATGGA-----GGGATATGATATATACCTTCAGATACTACAC	126	
QY	164	TGAAGAGTGGGGTCTGGAGACTTGTACTTCAACAAGAAACCCGTCTCCGGATGAAAA	223	
Db	127	CGAGGAAATGGGCTACAGGGGACTGTGACTTCATTAAGGAACCCGTGTTCCGTGAAGAAA	186	
QY	224	CGTCATTTTCATATGAAATCTTCCAGCCACCATGTACTTCATCATCTTGTGACTGGCAT	283	
Db	187	TGCTAATTTTCATATAAATCTTCTCGCCACCATCTACTCCATCTATCTTTTACTGGCAT	246	
QY	284	AGTGGCAATGGATTTGGTATCTGGTCATGGGTTTACAGAAAGATTAAGAGACATGAC	343	
Db	247	TGTGGCAATGGATTTGGTATCTGGTCATGGGTTTACAGAAAGATTAAGAGACATGAC	306	
QY	344	GGACAAGTACGGGCTGCACCTGTAGTGGCTGACCTCTCTTTGTCAATCACACTCCCTT	403	
Db	307	GGACAAGTACAGGGGTGACCTGTAGTGGGCGACCTCTCTTTGTCAATCACACTCCCTT	366	
QY	404	CTGGGCAATGATCCATGGCTGACTGTACTTTGGGAAATTTTGTGAAGGTGTCCA	463	
Db	367	CTGGGCAATGATCCATGGCTGACTGTACTTTGGGAAATTTTGTGAAGGTGTCCA	426	
QY	464	TATCATCTACACTGTCAACCTTACAGACAGCTTCTCATCTCGGCTTCATCAGCTGGA	523	
Db	427	TGTATCTACACTCAACCTTACAGACAGCTTCTCATCTCGGCTTCATCAGCTGGA	486	
QY	524	CCGGTACCTGGCCATTTGTCCAGGCGCACCAAGTCAAGTCAAGGCAAGGAAACTGGCGGCGA	583	
Db	487	CCGGTACCTGGCCATTTGTCCAGGCGCACCAAGTCAAGTCAAGGCAAGGAAACTGGCGGCGA	546	
QY	584	AAAGCAGTCTATGTGGGCGTCTGGATCCAGGCGCTCTCTGTACTATACCTGACTTCAT	643	
Db	547	AAAGTGTCTATGTGGGCGTCTGGATCCAGGCGCTCTCTGTACTATACCTGACTTCAT	606	
QY	644	CTTTGCCAGCTACGACCAAGGGGACATCAGTCAGGGGGATACAGGTAACATCTGTGACCG	703	
Db	607	CTTTGCCAGCTACGACCAAGGGGACATCAGTCAGGGGGATACAGGTAACATCTGTGACCG	651	
QY	704	CCTTACCCCGATTAAGCCTGTGGATGGTGGTCTTTCAATTCACAGATATATAGTGGGCT	763	
Db	652	CCTTACCCCGATTAAGCCTGTGGATGGTGGTCTTTCAATTCACAGATATATAGTGGGCT	711	
QY	764	CATCCTGGCCGCAATGCAATCTCTCTCTGTACTGCAATCATATCTTAAGCTGTGACA	823	
Db	712	TATCCTGCTGTATGTGCAATCTCTCTCTGTACTGCAATCATATCTTAAGCTGTGACA	771	
QY	824	CTTCAAGGGCCACGAGAACGCGACGCGCTTCAAGACGACAGTCACTCATCTAGCTTT	883	
Db	772	CTTCAAGGGCCACGAGAACGCGACGCGCTTCAAGACGACAGTCACTCATCTAGCTTT	831	
QY	884	CTTTGGCGTGGCGGCGCATTTTATGTGGGATAGAGTGAACGTCCTCATCTTTGGG	943	
Db	832	CTTTGGCGTGGCGGCGCATTTTATGTGGGATAGAGTGAACGTCCTCATCTTTGGG	891	
QY	944	AGTCATCAAGCAAGATGTGACTTCCAGAGAGATTTGTCACAAAGTGAATCTTCATACAGA	1003	
Db	892	AATCATCAAGCAAGAGGTGTGATTTGAAGAACGTCGTGACAAAGTGAATTCATACACGA	951	
QY	1004	GGCCCTGGCTTTCTTCCACTGTGTGCTGACCCCATCTTATGCTTTCTCTGGGGCCAA	1063	
Db	952	GGCCCTAGCTTTCTTCCACTGTGTGCTGACCCCATCTTATGCTTTCTCTGGGGCCAA	1011	

```
OY 1064 GTTCAAAAGCTCTGCCAGCATGACATCACTCACTGACAGAGAGGCTCCAGCTCAAGAT 1123
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1012 ATTTAAACCTCTGCCAGCAGCAGCATCTCTCTGACAGAGAGGCTCCAGCTCAAGAT 1071
OY 1124 CCTTTCAGAGAAAGGGGGGAGACTCTTCCGCTCTCCAGAGTCAAGATCTCCAG 1183
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1072 CCTCTCCAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1131
OY 1184 TTTTACCTCAGCTAACCTTATGCAAAAGCATATATATATATATATATATATATAT 1243
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1132 TTTTACCTCAGCTAACCTTATGCAAAAGCATATATATATATATATATATATATAT 1183
OY 1244 GAATTTTATGTTACACATTTTCCAGATATATATATATATATATATATATATATAT 1303
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1184 ACTTTTATGTTACACATTTTCCAGATATATATATATATATATATATATATATATAT 1243
OY 1304 TTTTATTTTATGTTACACATTTTCCAGATATATATATATATATATATATATATAT 1363
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1244 TATGCTGTTGATATATATATATATATATATATATATATATATATATATATATAT 1297
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 1364 TATTTATATATATATATATATATATATATATATATATATATATATATATATATAT 1423
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1298 GACTTATATATATATATATATATATATATATATATATATATATATATATATATAT 1353
OY 1424 GTGGCCAGCTTCTAGTACCTGTTATCTGTGTAGAGAGCTAGAGAGAGAGAGAGAG 1483
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1354 GTGGCCAGCTTCTAGTACCTGTTATCTGTGTAGAGAGAGCTAGAGAGAGAGAGAG 1405
OY 1484 AACTGAACTTCCAGATATGTTGTTAAATGTTAAAGTACCGGTGATCTCAGCTGTT 1543
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1406 AACTGAACTTCCAGATATGTTGTTAAATGTTAAAGTACCGGTGATCTCAGCTGTT 1465
OY 1544 GCTGCATA 1551
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1466 TATGCATA 1473

RESULT 8
AAA61656
ID AAA61656 standard; DNA; 1664 BP.
XX
AC AAA61656;
XX
DT 23-OCT-2000 (first entry)
XX
DE Human CXCR4 chemokine receptor (CXCR4) cDNA.
XX
KW CXCR4; human CXCR4 chemokine receptor 4; HIV infection inhibition;
expression inhibition; antisense therapy; ss.
OS Homo sapiens.
XX
FH Key location/Qualifiers
FT primer_bind 67..80
    /tag= a
    /bound_moiety= "Antisense oligonucleotide SEQ ID NO:1"
FT primer_bind 73..96
    /tag= b
    /bound_moiety= "Antisense oligonucleotide SEQ ID NO:2"
FT primer_bind 61..83
    /tag= b
    /bound_moiety= "Antisense oligonucleotide SEQ ID NO:3"
FT primer_bind 61..83
    /tag= b
    /bound_moiety= "Antisense oligonucleotide SEQ ID NO:3"
XX
XX WO2000031271-A1.
XX
XX 02-JUN-2000.
XX
XX 24-NOV-1999; 99WO-JP06534.
XX
XX 24-NOV-1998; 98JP-0332760.
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XX
PA (HISM ) HISAMITSU PHARM CO LTD.
XX
PI Iijima O, Goto T, Shimada T;
XX
DR WPI: 2000-400081/34.
XX
PT Antisense oligonucleotide, useful as inhibitor in preventive or remedy
for HIV infection with high therapeutic efficacy
XX
PS Example 1; Page 17-18; 21pp; Japanese.
XX
XX The invention relates to human CXCR4 chemokine receptor 4 (CXCR4)-specific
antisense oligonucleotides (AAA61652-AAA61654). The oligonucleotides
hybridise with the CXCR4 gene and/or CXCR4 RNA, thereby preventing its
expression. As CXCR4 plays a role in HIV infection, the antisense
oligonucleotides act as inhibitors of this process. Compositions
containing the antisense oligonucleotides are useful as prophylactic
or therapeutic agents for HIV infection. Such compositions are highly
effective for inhibiting infection with HIV. The present sequence
represents a human CXCR4 cDNA.
SQ Sequence 1664 BP; 414 A; 398 C; 359 G; 493 T; 0 other;
Query Match 50.7%; Score 951.8; DB 21; Length 1664;
Best Local Similarity 80.2%; Pred. No. 3.4e-170;
Matches 1209; Conservative 0; Mismatches 252; Indels 46; Gaps 6;
OY 45 CAGGTGCAAGTATGACAGTACCTCTGAGGCGTTTGCTGCTCCGTTACACCGAGCTGT 104
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 CGGACAGAGTATGACAAAGTACCGGAGGCGCTGAGTGTCTCCAGTACGACCGCATCTGG 60
OY 105 ACAGCAGAGTGTGCATGAGAACCGATCAGTGTGATATATATATATATATATATATATAT 164
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 AGAACACAGCGCTTACATGGA-----GGGATCAATATATATATATATATATATATATAT 115
OY 165 GAAGAAGTGGGCTGTGAGACTATGATCTCAACAAGAACCTGCTCCGGAGTGAAGAAC 224
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 116 GAGGAAGTGGGCTGTGAGACTATGATCTCAACAAGAACCTGCTCCGGAGTGAAGAAC 175
OY 225 GTCCATTTCAATAGATCTTCTGCGCCACATCTTATCATATCTTCTGATGCGGATTA 284
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 176 GCTAATTTCAATAAATCTTCTGCGCCACATCTTATCATATCTTCTTCAATGCGGAT 235
OY 285 GTGGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 344
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 236 GTGGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 295
OY 345 GACAGTACCGGCTGACCTGTCACTGAGTGGCTGCTCTCTTGTGATACACACTCCCTTC 404
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 296 GACAGTACCGGCTGACCTGTCACTGAGTGGCTGCTCTCTTGTGATACACACTCCCTTC 355
OY 405 TGGGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 464
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 356 TGGGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 415
OY 465 ATCATCTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 524
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 416 GTCATCTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 475
OY 525 CGGTACCTGCGCATTTGTCACAGCCCAACAAGTCAAGGCAAGGCAAGGCAAGGCAAGG 584
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 476 CGGTACCTGCGCATTTGTCACAGCCCAACAAGTCAAGGCAAGGCAAGGCAAGGCAAGG 535
OY 585 AAGGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 644
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 536 AAGGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 595
OY 645 TTTGCGCAGTACAGCAGGAGGAGGATCATGATGATGATGATGATGATGATGATGATGATG 704
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 596 TTTGCGCAGC-----TCAGTACGAGGAGATGATGATGATGATGATGATGATGATGATG 640
OY 705 CTTTACCCGATAGGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 764
```

Db	641	TTTACCCCAATGACTTGTGGGTGGTGTGTGTTCCAGTTTCAAGCATCATGATGGTGGCCTT	700
OY	765	ATCTGCCCGGCATGCTGATCTCTCTGTTTACTGCATCATCATCTGAAGCTGTCAAC	824
Db	701	ATCCTGCTGTGATATTGATCTCTGCTGCTAATGATATCATCTCCAAAGCTGTCAAC	760
OY	825	TCCAAAGGCGCCCGAAGGCCGAAGGCCCTCAAGACGACGATCATCTCATCTGCTTGC	884
Db	761	TTCCAAAGGCGCCCGAAGGCCGAAGGCCCTCAAGACGACGATCATCTCATCTGCTTGC	820
OY	885	TTTGCCTGCTGCTGCGCATATTTATGTGGGATGACATGACATGCACTCTCATCTTTGGGA	944
Db	821	TTGCGCTGTGGCTGTGCTTACTACATTTGGGATGACATGCACTCTCATCTTTGGGA	880
OY	945	GTCATCAAGCAAGGATGTGACTTTGAGAGACATTTGCAACAAGTGTATCTCCATCACAAG	1004
Db	881	ATCATCAAGCAAGGATGTGAGTTGAGAACACTGTGACACAGTGTGATTTCCATCACGAG	940
OY	1005	GCCCTGCGCTTCTTCCACTGTGCTCTGAACCCCATCTCTATGCTCTCTGGGCGCAAG	1064
Db	941	GCCCTGCGCTTCTTCCACTGTGCTCTGAACCCCATCTCTATGCTCTCTGGGCGCAAA	1000
OY	1065	TTCAAAAGCTGTGCCGACGATGACCTCACTCACTCCATGAGACAGAGGCTCAGCTCAAGATC	1124
Db	1001	TTTAAACCTGTGCCGACGACGACCTCACTCTCTGTGACAGAGGCTCAGCTCAAGATC	1060
OY	1125	CTTTCCAAAGGAAAGCGGGGTGACACTCTTCGCTCTCCACGAGATCGAATCTCCAGT	1184
Db	1061	CTTTCCAAAGGAAAGCGGGGTGACACTCTTCGCTCTCCACGAGATCGAATCTCCAGT	1120
OY	1185	TTTTCACATCCAGCTAACCTTATGCAAGACCTTATATATATATATATATATATATATAG	1244
Db	1121	TTTTCACATCCAGCTAACCTTATGCAAGACCTTATATATATATATATATATATATATAG	1172
OY	1245	AACCTTTTATGTATACACATTTTCCAGATATATAGAGACTGACGATCTGTACAGTTT	1304
Db	1173	CTTTTATTTAAGTTACACATTTTTCAGATATATATATATATATATATATATATATATAG	1232
OY	1305	TTTTTTTTTAAATGACTGTGGAGTTTATGTTCTCTAGTTTGTGAGGTTTGACTT	1364
Db	1233	ATTCCTGTTGGATTTTGTG-----CTGCTTTCTTAACTTTTGTGGAAGTTTAAATG	1286
OY	1365	AATTTATATATATATGTTTGTGTTGTTTTCATGATGATGACGCTTAGCGAGACCTG	1424
Db	1287	ACTTAT	1342
OY	1425	TGGCAGGCTTGTATGATGCTGTTATCTGTTGTAGAGCTTAAACCTGATAGAGAGAA	1484
Db	1343	TGGCAGGCTTGTATGATGCTGTTATCTGTTGTAGAGCTTAAACCTGATAGAGAGAA	1394
OY	1485	ACTCAACATTCACAAATGTTGTGTAATATGTAATGAAGCTAGCCGTTGATCTCAGCTGTTG	1544
Db	1395	ACTCAACATTCACAAATGTTGTGTAATATGTAATGAAGCTAGCCGTTGATCTCAGCTGTTG	1454
OY	1545	CTGCATA 1551	
Db	1455	ATGCATA 1461	
RESULT 9			
AA240014			
ID AA240014 standard; DNA; 1664 BP.			
AA240014;			
14-FEB-2000 (first entry)			
CXCR4 coding sequence.			
CXCR4; inhibitor; antisense oligonucleotide; anti-HIV agent;			
HIV infection; therapy; ss.			

OS	Synthetic.
XX	
PN	JP11285391-A.
XX	
PD	19-OCT-1999.
XX	
Pf	18-NOV-1996; 98UP-0327942.
XX	
PR	19-NOV-1997; 97JP-0335085.
XX	
PA	(HISM) HISAMITSU PHARM CO LTD.
PA	(TOAG) TOA GOSHI CHEM IND LTD.
XX	
DR	WPI: 2000-026817/03.
XX	
PT	An oligonucleotide used as an anti-HIV agent - inhibits CXCR4 protein expression
PS	Disclosure: Page 5-6; 6pp; Japanese.
CC	This sequence represents a CXCR4 coding sequence. The invention relates to antisense oligonucleotides that hybridise specifically with chromosomal DNA and/or RNA encoding a CXCR4 protein, and inhibit the expression of the CXCR4 protein. The antisense oligonucleotides can be used in an anti-HIV agent. The oligonucleotides and the anti-HIV agent are highly effective as a preventive and treating agent for HIV infection.
CC	
CC	
XX	
XX	
Seq	Sequence .1664 BP; 414 A; 398 C; 359 G; 493 T; 0 other;
Query Match	50.7%; Score 951.8; DB 21; Length 1664;
Best Local Similarity	80.2%; Pred. No. 3,4e-170;
Matches 1209; Conservative	0; Mismatches 252; Indels 46; Gaps 6
OY	45 CAGGTGCAGTAGACAGTACCCTTGAGGCGTTGGTGCTCCGGTAACCACCAAGCCTGTG 104 Db 1 CGGCGACGAGGTACGAAGAATGAGGCCGAGAGGCGCTGAGTGTCCAGTAGCCACCAGATTCTGG 60
OY	105 AGAGCGAGTGTTCCTCATCGAAGCCGATCAGTGTGAGTATATAACACTTCTGATAACTACTCT 164 Db 61 AGAACCCACGCGTTTACCATTGGA----GGGGATCACTATATATACACTTCAGATTAACAACC 115
OY	165 GAAGAAGTGGGGTCTGAGACATATACATTCACAAGAAAGAACCTGCTCCGGATTAANAAC 224 Db 116 GAGGAAATGGGCTCAGGGGACTATACATCACGAAGAAACCCTGTTCCGTGAAGAAAAT 175
OY	225 GTCCATTTCAAATAGAGATCTTCCTGCCCCACACATCTCATCATCATCTTCCTGTCAGGCATTA 284 Db 176 GCTAATTTCCAATAAATATCTTCCTGCCACACATCTCATCATCTTTCTTAATCTGGCAAT 235
OY	285 GTCCGCAATGATGATGTGATCCTGTCATCGGTTTACCAAGAAAGAAAGCTAAGAGCATGTACG 344 Db 236 GTGGGCATATGATTTGCTATCTCTGCTCATGGSTTTACCAAGAAAGAAAGCTAAGAGCATGTACG 295
OY	345 GACAAAGTACCGGCTGCACCTGTCAGTGGCTGACCTCTCTTTGTCATACACACTCCCCTTC 404 Db 296 GACAAGTACAGGCTGCACCTGTCAGTGGCCGACCTCTCTTTGTCATACAGGCTCCCTTC 355
OY	405 TGCGGAGTGAATGCCATGGGCTGACGTGATCACTTTGGGAAATTTTTGTGAAGGCTGTCAT 464 Db 356 TGGGGAGTTGATGCCCTGGCAACGTAATCTTTGGAACTTCTTAAGCAAGCAAGTATCAT 415
OY	465 ATCATATCATACAGTGTCAACCTCTACAGCAAGCGTTTCATACCTGGCCCTCATCAGCTGTGAC 524 Db 416 GTCATATCATACAGTGTCAACCTCTACAGCAAGTGTTCATACCTGGCCCTCATCAGTGTGAGC 475
OY	525 CGGTACTCTGCCAATGTCTCAGGCCACCAACAGTCAAAAGGCCAAGSAAAACTGCTGCGTGA 584 Db 476 CGGTACTCTGCCAATGTCTCAGGCCACCAACAGTCAAAAGGCCAAGSAAAACTGCTGCGTGA 535
OY	585 AAAGAGATCATATGTTGGGGCTGTGATATCCAGCCCTTCCTGACATATACCTGACTTCATC 644 Db 536 AAAGAGATCATATGTTGGGGCTGTGATATCCAGCCCTTCCTGACATATACCTGACTTCATC 595

OY	645	TTTTCCGACAGCAGCAGGCGGACATATCAGTACAGGAGGATGACAGTACATCTGTGACCG	704
Db	596	TTTTCCCAAG-----TCAGTAGGACAGTGCACATATATCTGTGACCGC	640
OY	705	CTTTACCCCGATAGCCTGTGATGATGGTGTGTTTCAATTTCCAGCATATATAGTGGGCTGC	764
Db	641	TTTACCCCAATGACTTCTGGGTGTGTTGTTCCAGTTTCAGACATCATCTGTGGCCTT	700
OY	765	ATCTGCCCCGATATGCTATCTCTCTCTGTTACTGACATCATATCTAGCTGTCAAC	824
Db	701	ATCTGCGCTGATATGTCATCTCTCTCTGCTTCGCTATTGACATTATCATCTCCAACTGTCAAC	760
OY	825	TCCAAAGGCCACAGAAAGCGAAGGCCCTCAAGACGACATCTCATCTCAAGCTTTC	884
Db	761	TCCAAAGGCCACAGAAAGCGAAGGCCCTCAAGACGACATCTCATCTGGCTTTC	820
OY	885	TTTTGCTGTGCTGCCATATATATGTGGGGATCAGATCGACTCTTCATCTTTTGGGA	944
Db	821	TTGCGCTGTGGTGTGCTTACTATATGGGATCGACATCGACTCTTCATCTGTGGAA	880
OY	945	GTCATCAAGCAGAGATGTGACTTGGAGAGCATTTGTGCACAAGTGGATCTCATACAGAG	1004
Db	881	ATCATCAAGCAGAGGCTGTGAATTTGAAGAACACTGTGCACAAGTGGATTTCCATCAACGAG	940
OY	1005	GCCCTGCGCTTCTTCACACTGTGTGCTGTAACCCCATCCGTATGCTTCCTGCGGGGCCAAG	1064
Db	941	GCCCTAGCTTTCTTCCACTGTGTGCTGTAACCCCATCTATAGCTTTCTTGGAGCCAA	1000
OY	1065	TTTCAAAAGCTTCGCCACGATGACACTCACTCACTCGATGAGCAGAGGCTCCAGCCTCAAGATC	1124
Db	1001	TTTAAAAACCTTCGCCACGACGACACTCACTCTGTGAGCAGAGGCTCCAGCCTCAAGATC	1060
OY	1125	CTTTCCAAAGAAAGCGGGGTGGACACTCTTCGCTTCACGGAGTCAGAATCTCTCACT	1184
Db	1061	CTTCCCAAGAAAGCGAGGTGGACATTCATCTGTTTCCACTGTGACTGTGACTCTTCAAGT	1120
OY	1185	TTTTACATCCAGCTAACCCCTTATGCAAAAGACTTATATATATATATATATATATGATTAAG	1244
Db	1121	TTTTACATCCAGCTAACCATGATGTAATAAGACTTTT-----TTTATACGATTAATAA	1172
OY	1245	AACCTTTTATATGTTACACATTTTCCAGATATTAAGACACTGCACAGCTTGTACAGTTTTT	1304
Db	1173	CTTTTATATAGTTATACACATTTTTCAGATATAAAGACTGCACATATATGTACAGTTTTT	1232
OY	1305	TTTTTTTTTTAATGACTGTGGGAGTTTATAGTTCCTCTAGTTTTTTTGGAGCTTTGACTT	1364
Db	1233	ATTTGCTGTGGATTTTGT-----CTGTGTTTCTTTTGTAGGATTTAATGTG	1286
OY	1365	AATTTATATATAATATGTTTGTGTTTCTTTGTTTTCATGTGATAGCGCTAGACAGACCTG	1424
Db	1287	ACTTATTTTATA-----TAATTTTTTTTTTTGTTTTCATATTTGATGTGTCTAGCAGACCTG	1342
OY	1425	TGGCCAAAGTCTTAGTACGTGTTTATCTGTGTGTAGGACTGTAGACGTGTAGAGGAAGAA	1484
Db	1343	TGGCCAAAGTCTTAGTACGTGTTTATCTGTGTGTGTAGGACTGTAGAGCTGTAGAGGA	1394
OY	1485	ACTGAACATTCACAGATGTGTGTAATTTGATATTAAGCTAGCGGTATCTCAGCTGTGG	1544
Db	1395	ACTGAACATTCACAGAGCGTGTAGTTAATTCAGCTAAAGCTAGAAATGATCCCAAGCTGTTT	1454
OY	1545	CTGCATA 1551	
Db	1455	ATGCATA 1461	

RESULT	10
ABK83803	
ID	ABK83803 standard; cDNA; 1670 BP.
XX	
AC	ABK83803;
XX	
DT	14-AUG-2002 (first entry)

Human cDNA differentially expressed in granulocytic cells #374.

Human: ss; granulocytic cell; DNA chip; bacterial infection; viral infection; parasitic infection; protozoal infection; fungal infection; sterile inflammatory disease; psoriasis; rheumatoid arthritis; glomerulonephritis; asthma; thrombosis; cardiac reperfusion injury; renal reperfusion injury; ARDS; adult respiratory distress syndrome; inflammatory bowel disease; Crohn's disease; ulcerative colitis; periodontal disease; granulocyte activation; chronic inflammation; allergy.

Homo sapiens.

WO200228999-A2.

11-APR-2002.

03-OCT-2001; 2001WO-US30821.

03-OCT-2000; 2000US-237189P.

(GENE-) GENE LOGIC INC.

Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J; WPI; 2002-435328/46.

Detecting granulocyte activation by detecting differential expression of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and drug toxicity

Claim 1; SEQ ID NO 374; 114pp; English.

The invention relates to detecting (M1) granulocyte (GC) activation (GCA), by detecting the level of expression of gene(s) (Gs) identified by DNA chip analysis as given in the specification, and comparing the expression level to an expression level in an unactivated GC, where differential expression of Gs is indicative of GCA.

Also included are modulating (M2) GA by contacting GC with an agent that alters the expression of at least one gene in Gs; (2) screening (M3) for an agent capable of modulating GCA or an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease using the gene expression profile; (3) detecting (M4) an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by detecting the level of expression in a sample of the tissue of gene(s) from Gs, where the level of expression of the gene is indicative of inflammation; (4) treating (M5) an inflammation (especially chronic) or in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by contacting a tissue having inflammation with an agent that modulates the expression of gene(s) from Gs in the tissue. M1 is useful for detecting GCA; M2 is useful for modulating GA; M3 is useful for screening an agent capable of modulating GCA preferably in an inflammation in a tissue; M4 is useful for detecting an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease (e.g. psoriasis, rheumatoid arthritis, glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal reperfusion injury, ARDS, adult respiratory distress syndrome, inflammatory bowel disease, Crohn's disease, ulcerative colitis, periodontal disease; also bacterial infection, viral infection, parasitic infection, protozoal infection, fungal infection and M5 is useful for treating one of the above conditions. The present sequence represents a gene differentially expressed in granulocytes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WPI at [ftp.wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences).

Sequence 1670 BP; 418 A; 400 C; 361 G; 491 T; 0 other;

Query Match 50.3%; Score 944.8; DB 24; Length 1670;
 Best Local Similarity 75.9%; Pred. No. 7,1e-169;
 Matches 1356; Conservative 0; Mismatches 297; Indels 133; Gaps 10;

OY 66 CTCTGAGGCGTTTGGTCTCGGTAAACACACGCGCTGTAGAGCGAGTGTGGCATGGA 125
 DB 18 CGCCGAGGCGCTGAGTGTCTCCAGTGCACCGCATCTGAGAACACGAGGGTATACCATGGA 77
 OY 126 CCGATCATGTGAGATATATACACTCTGTACTCTGTGAAGAAGTGGGCTGTGAAC 185
 DB 78 -----GGGATACAGATATATACACTCAACACACGAGGAATGGGCTCAGGGAC 132
 OY 186 TATGACTCCAAAGAAACCCCTGCTCGGATGAAAGCTCAATTTTAAATGATCTTC 245
 DB 133 TATGACTCCAAAGAAACCCCTGCTCGGATGAAAGCTCAATTTTAAATGATCTTC 192
 OY 246 CTGCCCCAATCTATCTATCATATCTTGTGACTGGCATAGTCGCAATGATGGTGTATC 305
 DB 193 CTGCCCCAATCTATCTATCATATCTTGTGACTGGCATAGTCGCAATGATGGTGTATC 252
 OY 306 CTGCTCATGGGTATACCAAGAAGTAAAGACATGAGGACATACCAGCTGACCTG 365
 DB 253 CTGCTCATGGGTATACCAAGAAGTAAAGACATGAGGACATACCAGCTGACCTG 312
 OY 366 TCAGTGGCTGACCTCCCTCTTGTCTACACACCTCCCTGCGGAGTTGATGCCATGGCT 425
 DB 313 TCAGTGGCTGACCTCCCTCTTGTCTACACACCTCCCTGCGGAGTTGATGCCATGGCT 372
 OY 426 GACTGTACTTGGGAAATTTTGTGTAAAGCTGTCCATATCATCTACACTGTCAACCTC 485
 DB 373 AACTGTACTTGGGAAATTTTGTGTAAAGCTGTCCATATCATCTACACTGTCAACCTC 432
 OY 486 TACACACCGTTCTATCTCTGCGCTTCTATCAGCCCTGACCGGTACCTGGCTTGTCCAC 545
 DB 433 TACACACCGTTCTATCTCTGCGCTTCTATCAGCCCTGACCGGTACCTGGCTTGTCCAC 492
 OY 546 GCCACCAACAGTCAAGAGGCAAGAACTGCTGAGTGAAGAGGAGCTATGTTGGGCTC 605
 DB 493 GCCACCAACAGTCAAGAGGCAAGAACTGCTGAGTGAAGAGGAGCTATGTTGGGCTC 552
 OY 606 TGGATCCAGCCCTCTCTCTGACTATATCTGACTTCACTCTTCCGACGTCAGCCAGGGG 665
 DB 553 TGGATCCAGCCCTCTCTCTGACTATATCTGACTTCACTCTTCCGACGTCAGCCAGGGG 601
 OY 666 GACATCATCAGGGGAGTGAAGATATCTGTGACCGCTTACCAGGATAGCTGTGG 725
 DB 602 ----TCAGTGAAGGAGTGAAGATATCTGTGACCGCTTACCAGGATAGCTGTGG 657
 OY 726 ATGTGTGTCTTCAATTCACAGATATATGTTGGTCTCAATCTCCGCGCATCTGTATC 785
 DB 658 GTGTGTGTCTTCAATTCACAGATATATGTTGGTCTCAATCTCCGCGCATCTGTATC 717
 OY 786 CTCTCTCTTACATCATCTCTTAAGCTGTCACTCTCAAGGCGCCACCAAGAGCGC 845
 DB 718 CTCTCTCTTACATCATCTCTTAAGCTGTCACTCTCAAGGCGCCACCAAGAGCGC 777
 OY 846 AAGGCGCTCAAGACACAGTCACTCTCACTGCTGCTTCTGCTGTTGGCTGCTTAC 905
 DB 778 AAGGCGCTCAAGACACAGTCACTCTCACTGCTGCTTCTGCTGTTGGCTGCTTAC 837
 OY 906 TATGTGGGATCAGCATGACATCTCTTCACTCTTGGGAGTCAAGCAAGAGTGTGAC 965
 DB 838 TATGTGGGATCAGCATGACATCTCTTCACTCTTGGGAGTCAAGCAAGAGTGTGAC 897
 OY 966 TTGAGAGCATTTGTCCACAGTGTATCTCATCAGAGAGGCGCTGCTTCTTCCACGT 1025
 DB 898 TTGAGAGCATTTGTCCACAGTGTATCTCATCAGAGAGGCGCTGCTTCTTCCACGT 957
 OY 1026 TGCCGTAAGCCCATCTCTATGCCCTCTCGGGGCGAGTCAAAAGCTCTGCCAGCAT 1085
 DB 958 TGCCGTAAGCCCATCTCTATGCCCTCTCGGGGCGAGTCAAAAGCTCTGCCAGCAT 1017

OY 1086 GCACCTCACTCCATGAGCAGAGGCTCCAGCCCTCAAGATCTTCCAAAGAAAGCGGGT 1145
 DB 1018 GCACCTCACTCCATGAGCAGAGGCTCCAGCCCTCAAGATCTTCCAAAGAAAGCGAGT 1077
 OY 1146 GCACCTCTCCGCTCCAGCAGAGTCAAGATCTCCAGTTTCTCACTCAAGCTTA 1205
 DB 1078 GCACCTCACTCCGCTCCAGCAGAGTCAAGATCTCCAGTTTCTCACTCAAGCTTA 1131
 OY 1206 TGCAAGACTAT 1265
 DB 1132 --CAGAGATGTAAGAGCTTTTATATATATATATATATATATATATATATATAT 1189
 OY 1266 TTCCAGAT 1325
 DB 1190 TTCCAGAT 1245
 OY 1326 GGGAGTTATATCTCTCTAGTTTGTGAGGTTTGCATTAATTAATTAATTAATTAAT 1385
 DB 1246 TGCTCTGTGTCTTGTATGTTTGTGAGGTTTAAATTAATTAATTAATTAATTAAT 1302
 OY 1386 TTGTTGTGTCTAT 1445
 DB 1303 TTTTGTGTCTAT 1362
 OY 1446 TTTATCTGTGTGTAGACTGTATGAGACTGTATGAGAAAGAACTTCCAGATGTGT 1505
 DB 1363 TATGTCTGTGTGTAGACTGTATGAGACTGTATGAGAAAGAACTTCCAGATGTGT 1414
 OY 1506 GGTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1565
 DB 1415 AGTGAATCACTGAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAAT 1473
 OY 1566 AGGACACCCACCCACCCACCCACCCACCCACCCACCCACCCACCCACCCACCCAC 1625
 DB 1474 ----- 1473
 OY 1626 GTGATGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTG 1685
 DB 1474 -----TTCCGCTGAAGCGTTTTCCTGTTTCAAGAGATTTTCTGTGAGAGATG 1526
 OY 1686 GCACCTTAATAAACCAAGCCTGAAGTGTGAGTGAAGTGTGAGTGTGAGTGTGAGTGT 1745
 DB 1527 GCACCTTAATAAACCAAGCCTGAAGTGTGAGTGAAGTGTGAGTGTGAGTGTGAG 1566
 OY 1746 TTTTTCAGTTTTCAGAGTATGATGACTTCACTCTCAACAAATGTATGATTTA 1805
 DB 1567 -TTTTCAGTTTTCAGAGTATGATGACTTCACTCTCAACAAATGTATGATTTA 1624
 OY 1806 CATCTTAATAAAGTCAATGATTAACCTTAATAAATAAATAAATAAATAAATAA 1851
 DB 1625 AGTTGTTAATAAAGTCAATGATTAACCTTAATAAATAAATAAATAAATAAATAA 1670

RESULT 11
 ABN95645
 ID ABN95645 standard; DNA; 1670 BP.
 AC ABN95645;
 DT 13-AUG-2002 (first entry)
 DE Gene #2143 used to diagnose liver cancer.
 XX
 KW Gene; liver cancer; ds; hepatocellular carcinoma; hepatotropic;
 KW metastatic liver tumour; cytostatic; expression profile; disease state;
 KW disease progression; drug toxicity; drug efficacy; drug metabolism.
 OS Homo sapiens.
 XX
 PN WO200229103-A2.
 PD 11-APR-2002.
 XX

OY		1686 GCACCTAAACAAGCCGTGAATGNGTGGTAAGAATCGTGSGGGTTTTTTTGTGTGTTG 1745
Dd		1527 GACATTATAACCAAAAGCCCCAAGTCgt-ATGAAAAATCCTGG-----1566
OY		1746 TTTTTCAGTTTCAGAGATGAGTTCAGTCAGTCCCACAAATGTCAGTCTGTATTA 1805
Dd		1567 -TTTTTCAGTTTCAGAGAGTGGGTGGTTGATTTCAGCACCTAC-AGGTTCACGCTTGATTA 1624
OY		1806 CATTGTTATATAAAAGTCATGATTAACCTTAAAAAAAAAAAAAAAAAAAAA 1851
Dd		1625 AGTTGTTATATAAAGTACATGTTAAACTTAAAAAAAAAAAAAAAAAAAAA 1670
PS	RESULT_12	
XX	AAKX15882	
AC	AAKX15882 standard; CDNA: 1944 BP.	
XX		
XX	AAKX15882;	
	12-MAY-1999 (first entry)	
DE	CDNA encoding G-protein coupled receptor polypeptide designated CXCR4B.	
KM	G-protein coupled receptor; CXCR4B; human; splice variant;	
KM	chemokine receptor; CXCR4; vaccine; gene therapy; HIV-1; HIV-1;	
KM	cancer; pain; diabetes; obesity; anorexia; bulimia; asthma;	
KM	Parkinson's disease; acute heart failure; hypotension; hypertension;	
KM	urinary retention; osteoporosis; angina pectoris; myocardial infarction;	
KM	stroke; ulcer; allergy; benign prostatic hypertrophy; migraine;	
KM	vomiting; psychotic disorder; neurological disorder; anxiety;	
KM	schizophrenia; manic depression; delirium; dementia; mental retardation;	
KM	dyslexias; Huntingtons disease; Gilles de la Tourette syndrome; ss.	
OS	Homo sapiens.	
XX		
FH	Key Location/Qualifiers	
FT	CDS 336..1406	
FT	/tag= a	
FT	misc-feature 361	
FT	/tag= b	
FT	/note= "splice acceptor site"	
XX		
PN	EP897980-A2.	
PD	24-FEB-1999.	
XX		
XX	07-AUG-1998; 98EP-0306324.	
PR	24-JUL-1998; 98US-0056601.	
XX	20-AUG-1997; 97US-0056601.	
PA	(SMIK) SMIHKLINE BEECHAM CORP.	
PI	Gupta SK, Pillarisetti K;	
DR	WPI: 1999-134643/12.	
XX	P-PDB: AAW97362.	
PT	New G protein coupled receptor (CXCR4B) polypeptide and	
PT	polynucleotide, human splice variant of a chemokine receptor -	
PT	useful as diagnostic reagents and for prevention and treatment of	
XX	HIV infection, cancer, stroke and dementia	
XX		
PS	Claim 2; Page 16-17; 2app; English.	
XX		
CC	The present sequence encodes a G-protein coupled receptor polypeptide	
CC	designated CXCR4B, which is a human splice variant of a chemokine	
CC	receptor CXCR4. CXCR4B polynucleotides and polypeptides are useful for	
CC	diagnosing susceptibility to diseases by detecting mutations or	
CC	polymorphisms in the CXCR4B gene or analysing for the presence or amount	
CC	of CXCR4B polypeptide expressed in a patient. CXCR4B polypeptides and	
CC	polynucleotides are also useful for screening for antagonists and	

CC	agonists which can be used to treat conditions associated with CXCR4B
CC	polypeptide imbalance. CXCR4B polypeptides can be administered directly
CC	(as a vaccine) or via a vector (gene therapy) to prevent disease.
CC	Diseases diagnosed, prevented and treated include: HIV-1 and HIV-1
CC	infections; cancer; pain; diabetes; obesity; anorexia; bulimia; asthma;
CC	Parkinson's disease; acute heart failure; hypotension; hypertension;
CC	urinary retention; osteoporosis; angina pectoris; myocardial infarction;
CC	stroke; ulcers; allergies; benign prostatic hypertrophy; migraine;
CC	vomiting; psychotic and neurological disorders, including anxiety,
CC	schizophrenia, manic depression, delirium, dementia and severe mental
CC	retardation and dyskinesias, such as Huntington's disease or Gilles de
CC	la Tourette syndrome. CXCR4B polypeptides are useful for mapping genes
CC	to chromosomes, allowing gene inheritance to be studied through linkage
CC	analysis.
XX	
XX	
Sequence	1944 BP; 497 A; 437 C; 412 G; 596 T; 2 other;
Query Match	50.1%; Score 939.8; DB 20; Length 1944;
Best Local Similarity	76.4%; Freq. No. 6.5e-168;
Matches 1131:	Conservative 2; Mismatches 274; Indels 130; Gaps 8;
QY	134 TGTGAGTATATACACTTCTGATTAATCTAGAGAGAGTGGGCTGAGACATCTGATCTC 193
DB	111
	356 TTTCGACGATATACACTTCTGATTAATCTAGAGAGAGTGGGCTGAGACATCTGATCTC 415
QY	194 CAACAGGAACCCCTGCTCCCGGGATGAAAACGTCATTTCAATAGATCTCTCCGCCAAC 253
DB	111
	416 CATGAGGAACCCCTGCTCCCGGGATGAAAACGTCATTTCAATAGATCTCTCCGCCAAC 475
QY	254 CATCTACTTCATCATCTTCTTGACTGGCATGTGGGCAATGATGGTATCTGTGATCT 313
DB	111
	476 CATCTACTTCATCATCTTCTTGACTGGCATGTGGGCAATGATGGTATCTGTGATCT 535
QY	314 GGGTTACAGAAAGCCTAAGGACATGACGCAAGACGAGCGGTGACACCTGTAGAGGC 373
DB	111
	536 GGGTTACAGAAAGCCTAAGGACATGACGCAAGACGAGCGGTGACACCTGTAGAGGC 595
QY	374 TGACCTCCTCTTGTGCATCACATCCCTCTTGAGGAGTTGATGATGAGTCACTGCTA 433
DB	111
	596 CGACCTCCTCTTGTGCATCACATCCCTCTTGAGGAGTTGATGATGAGTCACTGCTA 655
QY	434 CTTTGGGAATTTTGTGTGAAGGCTGTCCATATCATCTACATGTCACACCTCTACAG 493
DB	111
	656 CTTTGGGAATTTTGTGTGAAGGCTGTCCATATCATCTACATGTCACACCTCTACAG 715
QY	494 CGTTCTCATCTGCGCTTCATCAGCCGTGAGACCGTACTCGCCATTTGTCCAGCCACCA 553
DB	111
	716 TGTCTCTCATCTGCGCTTCATCAGCCGTGAGACCGTACTCGCCATTTGTCCAGCCACCA 775
QY	554 CAGTCAAGGCCAAGAAATGTGTGGCTGAAAAGGACATCTATGTGGGCGCTGGATGCC 613
DB	111
	776 CAGTCAAGGCCAAGAAATGTGTGGCTGAAAAGGACATCTATGTGGGCGCTGGATGCC 835
QY	614 AGCCCTCCTCTGACTATACCTGACTTCATCTTTGCCAGCGTCACGCAAGGCGGACATCAG 673
DB	111
	836 TGCCCTCCTCTGACTATACCTGACTTCATCTTTGCCAGCGTCACGCAAGGCGGACATCAG 880
QY	674 TCAGGGGATACAGGTCATCTGTGACCGCGCTTTACCCCGATAGCCTGTGTGATGTGCT 733
DB	111
	881 TGAGGCAATACAGGTCATCTGTGACCGCGCTTTACCCCGATAGCCTGTGTGATGTGCT 940
QY	734 GTTTCATATTCAGCAATATATGTGGGCTGTATCTGCGCGGATATGTCATCTCTCTG 793
DB	111
	941 GTTTCATATTCAGCAATATATGTGGGCTGTATCTGCGCGGATATGTCATCTCTCTG 1000
QY	794 TTACTGCATCATCTCTAGCTGTGCACATCCAAAGGGCCACCAAGAGGCAAGGCGCT 853
DB	111
	1001 CTATTCGATTTATCATCTCTCAAGGCTGTGCACATCCAAAGGGCCACCAAGAGGCAAGGCGCT 1060
QY	854 CAAGAAGCACTCATCTCATCTGAGCTTTCTTTGCTGCTGCTGCTGCCATATTTATGTGG 913
DB	111
	1061 CAAGAAGCACTCATCTCATCTGAGCTTTCTTTGCTGCTGCTGCTGCCATATTTATGTGG 1120

Query Match 49.8%; Score 934; DB 21; Length 5161;
Best Local Similarity 81.6%; Pred. No. 1e-166;
Matches 1157; Conservative 0; Mismatches 220; Indels 41; Gaps 5;

134 TGTGATATATACCTTCTGATTAATCTGAGAGAGTGGGCTCGAGACTATGACTC 193
13178 TTGGAGATATACCTTCTGATTAATCTGAGAGAGTGGGCTCGAGACTATGACTC 3237
194 CAG 253
3238 CATTGAG 3297
254 CATTGAG 313
3298 CATTGAG 3357
314 GGGTTACCAAG 373
3358 GGGTTACCAAG 3417
374 TGACCTCTCTTGTGATCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 433
3418 CGACCTCTCTTGTGATCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3477
434 CTTTGGGAAATTTTGTGATCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 493
3478 CTTTGGGAAATTTTGTGATCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3537
494 CTTTGGGAAATTTTGTGATCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 553
3538 TGTCTGATCAG 3597
554 CAGTCAAG 613
3598 CAGTCAAG 3657
614 AGCCCTCTCTTGTGATCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 673
3658 TGTCTGATCAG 3702
674 TCAAG 733
3703 TCAAG 3762
734 CATTGAG 793
3763 CATTGAG 3822
794 TCAAG 853
3823 CATTGAG 3882
854 CAG 913
3883 CAG 3942
914 CATTGAG 973
3943 CATTGAG 4002
974 CATTGAG 1033
4003 CATTGAG 4062
1034 CATTGAG 1093
4063 CATTGAG 4122
1094 CATTGAG 1153
4123 CATTGAG 4182
1154 TTTGCTCTCTGATCAG 1213

4183 ATCTGTTTCCAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 4234
1214 CTTAT 1273
4235 TGTAAAG 4294
1274 ATAAAG 1333
4295 ATAAAG 4348
1334 ATGTTCTCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1393
4349 GGTGTTCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 4404
1394 TTTGATGAG 1453
4405 TTTGATGAG 4464
1454 TGTGAG 1513
4465 GTGTAAG 4516
1514 GATTAAG 1551
4517 AGGTAAG 4554

RESULT 15
AAA34774
ID AAA34774 standard; DNA; 5161 BP.
XX
AC AAA34774;
XX
DT 28-JUL-2000 (first entry)
XX
DE Human adenosine receptor related polynucleotide SEQ ID NO:2463.
XX
KW Human; adenosine receptor; low adenosine antisense oligonucleotide;
XX phosphorothioate; impaired respiration; inflammation; allergy;
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW antiallergic; antischistosomal; cytostatic; analgesic; impaired airway;
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX
OS Homo sapiens.
XX
PN WO200009525-A2.
XX
PD 24-FEB-2000.
XX
PE 03-AUG-1999; 99WO-US17712.
XX
PR 03-AUG-1998; 98US-0095212.
XX
PA (UYEC-) UNIV EAST CAROLINA.
XX
PI Nyce JW;
XX
DR WPI; 2000-205971/18.
XX
PT New antisense oligonucleotides useful for treating e.g. pulmonary
PT vasoconstriction, inflammation, allergies, asthma, hypertension,
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT cancers
XX
PS Disclosure: Page 600-601; 1343pp; English.
XX
CC The present invention describes a new composition comprising an
CC antisense oligonucleotide (ON) with low adenosine (up to 15%), which
CC targets nucleic acids involved in bronchoconstriction, allergies, and/or

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OM nucleic - nucleic search, using sw model

Run on: July 12, 2003, 14:24:28 ; Search time 74 Seconds
(without alignments)
7778.815 Million cell updates/sec

Title: US-09-367-052-1
Perfect score: 1877
Sequence: 1 ccacccaatacagactcact.....aaaaaaaaaaaaaaaaaa 1877

Scoring table: IDENTITY NUC
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Searched: 441362 seqs, 153338381 residues
number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	974.4	51.9	1737	1	US-08-202-056-4
2	974.4	51.9	1737	1	US-08-076-093A-3
3	974.4	51.9	1737	1	US-08-701-265-3
4	974.4	51.9	1737	2	US-08-284-586-3
5	974.4	51.9	1737	2	US-08-805-478-3
6	974.4	51.9	1737	2	US-08-802-627A-3
7	974.4	51.9	1737	2	US-08-801-238-3
8	974.4	51.9	1737	2	US-08-801-228-3
9	974.4	51.9	1737	3	US-09-104-296-3
10	974.4	51.9	1737	3	PCT-US94-06380-2
11	952.8	50.8	1679	4	US-09-517-605-14
12	951.8	50.7	1664	4	US-09-582-224A-5
13	834.6	44.5	1317	1	US-08-153-848-45
14	834.6	44.5	1317	3	US-09-299-843A-45
15	834.6	44.5	1317	3	US-09-088-337B-45
16	834.6	44.5	1317	5	PCT-US93-11153-45
17	198.4	10.6	1679	1	US-08-202-056-6
18	198.4	10.6	1679	1	US-08-076-093A-5
19	198.4	10.6	1679	1	US-08-701-265-5
20	198.4	10.6	1679	2	US-08-284-586-5
21	198.4	10.6	1679	2	US-08-805-478-5
22	198.4	10.6	1679	2	US-08-802-627A-5
23	198.4	10.6	1679	2	US-08-801-238-5
24	198.4	10.6	1679	2	US-08-801-228-5
25	198.4	10.6	1679	3	US-09-104-296-5
26	198.4	10.6	1679	3	PCT-US94-06380-3
27	198.4	10.6	2818	3	US-08-982-493-7

28	198.4	10.6	2818	4	US-08-628-655-1	Sequence 1, Appli
29	195.8	10.4	2085	3	US-09-299-843A-65	Sequence 65, Appl
30	195.8	10.3	1670	4	US-08-829-838-1	Sequence 1, Appli
31	193.8	10.3	1670	4	US-08-829-838-1	Sequence 1, Appli
32	193.8	10.3	1670	4	US-08-829-838-1	Sequence 1, Appli
33	186.8	10.0	2751	1	US-08-153-848-23	Sequence 23, Appl
34	186.8	10.0	2751	3	US-09-299-843A-23	Sequence 23, Appl
35	186.8	10.0	2751	4	US-09-088-337B-23	Sequence 23, Appl
36	186.8	10.0	2751	4	PCT-US93-11153-23	Sequence 23, Appl
37	183.8	9.8	1373	5	PCT-US92-02977-6	Sequence 6, Appli
38	183.8	9.8	1373	5	PCT-US95-03032-3	Sequence 3, Appli
39	182	9.7	1900	1	US-08-153-848-18	Sequence 18, Appl
40	182	9.7	1900	4	US-09-299-843A-18	Sequence 18, Appl
41	182	9.7	1900	4	US-09-088-337B-18	Sequence 18, Appl
42	182	9.7	1900	5	PCT-US93-11153-18	Sequence 18, Appl
43	182	9.7	2058	1	US-08-153-848-6	Sequence 6, Appli
44	182	9.7	2058	3	US-09-299-843A-6	Sequence 6, Appli
45	182	9.7	2058	4	US-09-088-337B-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-08-202-056-4
; Sequence 4, Application US/08202056
; Patent No. 5440021
; GENERAL INFORMATION:
; APPLICANT: Chantharapai, Anan
; APPLICANT: Hebert, Caroline
; APPLICANT: Kim, Kyung Jin
; APPLICANT: Lee, James
; TITLE OF INVENTION: Antibodies to Human IL-8 Type B Receptor
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: path (genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/202,056
; FILING DATE: 25-FEB-1994
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/677211
; FILING DATE: 29-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: 706P3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1737 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-202-056-4

Query Match 51.9%; Score 974.4; DB 1; Length 1737;
Best Local Similarity 76.1%; Pred. No. 2.1e-187;
Matches 1391; Conservative 0; Mismatches 301; Indels 136; Gaps 10;

OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WinPatIn (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/076,093A
 FILING DATE: 11-Jun-1993
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/810782
 FILING DATE: 19-DEC-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/677211
 FILING DATE: 29-MAR-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Love, Richard B
 REGISTRATION NUMBER: 34,659
 REFERENCE/DOCKET NUMBER: 706P2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415/225-5530
 TELEFAX: 415/952-9881
 TELEX: 910/371-7168
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1737 nucleotides
 TYPE: Nucleic Acid
 STRANDEDNESS: Single
 TOPOLOGY: Linear
 US-08-076-093A-3

Query Match 51.9%; Score 974.4; DB 1; Length 1737;
 Best Local Similarity 76.1%; Pred. No. 2,1e-187;
 Matches 1391; Conservative 0; Mismatches 301; Indels 136; Gaps 10;

50 GCAGGAGCAGGACCCCTGTCGAGGCGTTGGTCTCCGCTAACCCAGCGGTGAGAC 109
 20 GCGCGCGCGAAGTACGCGCGGCGCTGAGTCTCCAGTACGCGCGCATCTGGAGAC 79
 110 GAGTGTGCGCATGGAACCGATCATGTGATATATACACTTCTGATTAAGTCTGAGA 169
 80 CAGCGGTTACATGGA-----GGGGATCAGTATATACACTTCAGATTAAGTCTGAGA 134
 170 AGTGGGCTGTCGAGACATGATCTCCAAACAGGACCCCTGTCGAGGATGAGAAAGTCA 229
 135 AATGGGCTCAGGCGATGATGACTCATGAAGAACCTTTCCGGAAGAAATGCTAA 194
 230 TTTCATAGGATCTTCGCGCCACCATCATCTTCATCTTCATCTGACGTGATAGTGG 289
 195 TTTCATTAATAATCTTCGCGCCACCATCATCTTCATCTTCATCTGACGTGATAGTGG 254
 290 CAATGATGATGATCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 349
 255 CAATGATGATGATCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 314
 350 GTCACGGCTGTCACGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 409
 315 GTCACGGCTGTCACGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 374
 410 AGTGTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 469
 375 AGTGTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 434
 470 CTACACTGTCAACCTCTACAGCAGGCTTCTCATCTGTCGTCGTCGTCGTCGTCGTCGTC 529
 435 CTACACTGTCAACCTCTACAGCAGGCTTCTCATCTGTCGTCGTCGTCGTCGTCGTCGTC 494
 530 CCTGCGCATTTGTCACGCGCCACCAACAGTAAAGGCCAAGGAGGAGGAGGAGGAGGAGG 589
 495 CCTGCGCATTTGTCACGCGCCACCAACAGTAAAGGCCAAGGAGGAGGAGGAGGAGGAGG 554
 590 AGTGTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 649
 555 GGTCTATGTTGGGCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 614
 650 CGAGCTCAGCCAGGGGAGCATGTCAGGGGAGTGAAGGAGTGAAGTGAAGTGAAGTGAAGT 709

615 CAACG-----TCAGTACGACATGACATATATCTGACCGCTTCA 659
 710 CCCCATGACCTGTCGATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 769
 660 CCCCATGACCTGTCGATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 719
 770 GCGCGGATCATCT 829
 720 GCGCGGATCATCT 779
 830 GCGCGGATCATCT 889
 780 GCGCGGATCATCT 839
 890 CTGCTGCTGTCAT 949
 840 CTGCTGCTGTCAT 899
 950 CAAGCAGGATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 1009
 900 CAAGCAGGATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 959
 1010 GCGCTTCTTCACTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 1069
 960 GCGCTTCTTCACTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 1019
 1070 AAGCTCTGCGCAGATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 1129
 1020 AAGCTCTGCGCAGATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 1079
 1130 CAAGCAGGATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 1189
 1080 CAAGCAGGATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 1139
 1190 CTGCAAGTAACTTATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 1249
 1140 CTGCAAGTAACTTATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 1199
 1250 TTTTATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 1309
 1192 TTTTATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 1251
 1310 TTTTATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 1369
 1252 TTTTATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 1305
 1370 AT 1429
 1306 TTTTAT 1361
 1430 AAGTCTTATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 1489
 1362 AAGTCTTATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 1413
 1490 ACATTCAGAAATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 1549
 1414 ACATTCAGAAATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 1473
 1550 TATCTCTTCAATTCGAGGAGCAGCCACCCACCCACCCACCCACCCACCCACCCACCCATCTTA 1609
 1474 TAGATATATCTTCA----- 1488
 1610 TGTGTTGTTATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 1669
 1489 -----TTCCCGTGAAGCTTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1525
 1670 TTTTCTGTAAGATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 1729
 1526 TTTTCTGTAAGATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 1581
 1730 TTTTCTGTAAGATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 1789

Db 1582 -----TTTTTCAGTTTTTCAGAGTGGGTGATTTTCAGCACTAC-AGT 1623

QY 1790 GTACAGCTCTGTATTCATTGTTAATAAGTCATATTAACCTTAATAAAAAA 1849

Db 1624 GTACAGCTCTGTATTCATTGTTAATAAGTCATATTAACCTTAATAAAAAA 1683

QY 1850 AAAAAAAAAAAAAAAAAAAAAAAAAA 1877

Db 1684 AAAAAAAAAAAAAAAAAAAAAAAAAA 1711

RESULT 3

US-08-701-265-3

Sequence 3, Application US/08701265

Patent No. 5776457

GENERAL INFORMATION:

APPLICANT: Chuntarapat, Anan

APPLICANT: Lee, James

APPLICANT: Hebert, Caroline

APPLICANT: Jin Kim, K.

TITLE OF INVENTION: Antibodies to Human PFA4 Receptors

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 460 Point San Bruno Blvd

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 Inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Winpatin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/701,265

FILING DATE: 22-AUG-1996

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/076093

FILING DATE: 11-Jun-1993

APPLICATION NUMBER: 07/810782

FILING DATE: 19-DEC-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/677211

FILING DATE: 29-MAR-1991

ATTORNEY/AGENT INFORMATION:

NAME: Love, Richard B

REGISTRATION NUMBER: 34,659

REFERENCE/DOCKET NUMBER: 706B2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415/425-5530

TELEFAX: 415/952-9881

TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 1737 nucleotides

TYPE: Nucleic Acid

STRANDEDNESS: Single

TOPOLOGY: Linear

US-08-701-265-3

Query Match 51.9%; Score 974.4; DB 1: Length 1737;

Best local Similarity 76.1%; Pred. No. 2,1e-187;

Matches 1391; Conservative 0; Mismatches 301; Indels 136; Gaps 10;

QY 50 GCAGGTAGAGTACCCCTCTGAGGCGTTTGTCTCCGTAACCAACGAGGCTGTAGAC 109

Db 20 GCGGCGCGAAGTAGAGCGCGGCGCTGAGTCTCCAGTAGCAGCGCATCTGGAGAC 79

QY 110 GAGGTGTCATGAGAACCATCAGTGTGATATATACCTTCTGATTAATCTACTGAGAG 169

Db 80 CAGCGGTACCATGGA-----GGGATCAGATATATACCTTCTGATTAATCTACTGAGAG 134

QY 170 AGTGGGCTGTGAGACTATGACTCCACAGGAGACCTGCTCCGGATGAAGAGCTCA 229

Db 135 AATGGGCTGAGGAGTATGACTCCATGAGAGAGACCTGCTCCGTAAGAGAAATGCTAA 194

QY 230 TTTCAATAGGATCTTCTGCGCCAGCATCTTCTATCATCTTCTTACTGAGCATAGTGG 289

Db 195 TTTCAATAGGATCTTCTGCGCCAGCATCTTCTATCATCTTCTTACTGAGCATAGTGG 254

QY 290 CAATGATGATGATCTTCTGCGCCAGCATCTTCTATCATCTTCTTACTGAGCATAGTGG 349

Db 255 CAATGATGATGATCTTCTGCGCCAGCATCTTCTATCATCTTCTTACTGAGCATAGTGG 314

QY 350 GTACCGGCTGACACCTGTCAGTGGTACCTCTCTTGTGATCAGATCCCTCTGAGGC 409

Db 315 GTACAGGCTGACACCTGTCAGTGGTACCTCTCTTGTGATCAGATCCCTCTGAGGC 374

QY 410 AGTTGATGCGCATGCTGATGCTGATCTTGGAAATTTTGTGTAAGGCTGTCCATATAT 469

Db 375 AGTTGATGCGCGTGAAGTATGCTGATCTTGGAAATTTTGTGTAAGGCTGTCCATATAT 434

QY 470 CTACAGTGTCAACCTCTTACAGAGGCTTCTATCTGCGCTTCTATCAGCTGAGCGGTA 529

Db 435 CTACAGAGTCAACCTCTTACAGAGGCTTCTATCTGCGCTTCTATCAGCTGAGCGGTA 494

QY 530 CTTGCGCATGTCACAGCGCCACCAAGAGTCAAGGCAAGGCAAGGCAAGGCAAGGCA 589

Db 495 CTTGCGCATGTCACAGCGCCACCAAGAGTCAAGGCAAGGCAAGGCAAGGCAAGGCA 554

QY 590 AGTCTATGTTGGGCTGTGATGCTCCAGCCCTCTCTCTGATATATCTGATCTATCTTTC 649

Db 555 GGTCTATGTTGGGCTGTGATGCTCCAGCCCTCTCTCTGATATATCTGATCTATCTTTC 614

QY 650 CCAGCTGACAGCGAGGAGATGATGATGAGGAGTACAGATGATCTGATGAGCGCTTTA 709

Db 615 CAAG-----TCAGTGAAGCAGATGATGATGATGATGATGATGATGATGATGATG 659

QY 710 CCCGATGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 769

Db 660 CCCGATGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 719

QY 770 GCGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 829

Db 720 GCGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 779

QY 830 GCGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 889

Db 780 GCGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 839

QY 890 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 949

Db 840 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 899

QY 950 CAAGCAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1009

Db 900 CAAGCAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 959

QY 1010 GCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1069

Db 960 GCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1019

QY 1070 AAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1129

Db 1020 AAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1079

QY 1130 CAAGGAAAGCGGGGTGACACTCTTCCGTCACAGGAGTGAAGATCCCTCAGTTTCA 1189

Db 1080 CAAGGAAAGCGGGGTGACACTCTTCCGTCACAGGAGTGAAGATCCCTCAGTTTCA 1139

QY 1190 CTTCAGCTTACCTTATGCAAGACTTATATATATATATATATATATATATATATAT 1249

Db 1140 CTTCAGCTTACCTTATGCAAGACTTATATATATATATATATATATATATATATAT 1199

QY 1250 TTTATGTTACACATTTTCCAGATATAGAGACTGACAGTCTTGTACAGTTTATTTT 1309
DB 1192 TTTTAACTTACACATTTTTCAGATATATAAGAGTACCAATATATGACAGTTTATTTG 1251
QY 1310 TTTTAAATGACCTGTGGAGATTTATGTCCTCTAGTTTGTAGAGTTTACTTAATTT 1369
DB 1252 TTTGTTGATTTTGT-----CTTGCTGTTTGTAGTTTGTAGAGTTTATTTGACTTA 1305
QY 1370 ATATAAATATGTTTGTGTTTGTTCATGTAATGAGCGCTGTAGCGAGCACTGTGGCC 1429
DB 1306 TTTTATA-----TAATTTTTTTTTTTGTTTCATATGATGTGTCTAGCGAGCACTGTGGCC 1361
QY 1430 AAGTCTTAGTAGCTGTTTATCTGTGTAGAGCTGTAGAACTGTAGAGAAACTGA 1489
DB 1362 AAGTCTTAGTAGCTGTTATGCTGTGTAGAGCTGTAGAA-----AAGGGAATGA 1413
QY 1490 ACATTCAGATGTGTGTAATGTAATGAAGAGTAGCCGTATCTCAGCTGTGCTGCA 1549
DB 1414 ACATTCAGAGCGGTGTAGTGAATACGTAAGAGTAAGTAATATCCCGAGCTGTATGCA 1473
QY 1550 TAATCTCTCATTTCCGAGAGACACCCACCCACCCACCCACCCACCCCACTTCTTAAT 1609
DB 1474 TAGATATCTCTGCA----- 1488
QY 1610 TGTGTTGTTATGCTGTGATGTTGTTGTTTGTGTTGTTGTTGTTGTTGTTT 1669
DB 1489 -----TTCCCGTGAACGTTTCCGTGTTCTTAAGAGCTGAT 1525
QY 1670 TTTTCTGTAAAGATGACACTTAAACCAAGCCTGAAATGTGTAGAAATGCTGGGGT 1729
DB 1526 TTTCTGTAGAGATGACACTTAAACCAAGCCTGAAATGTGTAGAAATGCTGGGGT 1581
QY 1730 TTTTGTGTTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGT 1789
DB 1582 -----TTTTCAGTTTTCAGAGAGTGTGTTGATTTTCAGCACTTAC 1623
QY 1790 GTACAGTCTGTATTAATGTTTAAATAAGCTCAATGTAATGTTAAATAAGCTTAA 1849
DB 1624 GTACAGTCTGTATTAATGTTTAAATAAGCTCAATGTTAAATAAGCTTAAATAAG 1683
QY 1850 AAAAAAAAAAAAAAAAAAAAAAAAAA 1877
DB 1684 AAAAAAAAAAAAAAAAAAAAAAAAAA 1711

RESULT 4
US-08-284-586-3
Sequence 3, Application US/08284586
Client No. 5840856
GENERAL INFORMATION:
APPLICANT: Chunharapal, Anan
APPLICANT: Lee, James
APPLICANT: Hebert, Caroline
APPLICANT: Jin Kim, K.
TITLE OF INVENTION: Antibodies to Human PFA Receptors
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/284,586
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/076, 093A
FILING DATE: 11-Jun-1993
APPLICATION NUMBER: 07/810782
FILING DATE: 19-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/677211
FILING DATE: 29-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 706P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
TELEX: 910/371-7168
SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO: 3:
LENGTH: 1737 nucleotides
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
US-08-284-586-3

Query Match 51.9%; Score 974.4; DB 2; Length 1737;
Best Local Similarity 76.1%; Pred. No. 2,1e-187;
Matches 1391; Conservative 0; Mismatches 301; Indels 136; Gaps 10;

QY 50 GCAGGTACAGTACACCTCTGAGGCGTTTGGTGTCTCCGGGTATACCAACCAAGCGCTGAGAGC 109
DB 20 GCGGCGCGCAAAAGTACCGCGAGGCGCTGAGTGTCCAGTCCAGCCATCTGTGAGAC 79
QY 110 GAGTGTCCCAATGGAACGATGAGTATATATACACTTCTGTACTACTCTGAAGA 169
DB 80 CAGCGGTACCATGGA-----GGGATCAGTATATACACTTCAATACCTACCGAGGA 134
QY 170 AGTGGGTCTGAGACTATGACTCCACAGAAACCTGCTCCGGGATGAAGAGCTGCA 229
DB 135 AATGGGCTCAGGGGACTATGACTCATGAAGAAACCTGTTCCGTGAAGAAAGCTAA 194
QY 230 TTTCAATAGGATCTTCCCTGCCACCATCTACTTATCATCTTCTTGAAGCTGATGCTGG 289
DB 195 TTTCAATAAATCTTCCCTGCCACCATCTACTTCAATCTTCTTGAAGCTGATGCTGG 254
QY 290 CAATGATTTGTTGATCTGTGATGAGGTTTACAGAGAAGCTAAGAGCATGACGAGCAA 349
DB 255 CAATGATTTGTTGATCTGTGATGAGGTTTACAGAGAAGCTAAGAGCATGACGAGCAA 314
QY 350 GTACGCTGACACTGTGAGTGGCTGACCTCTCTTGTGATCAGACCTCCCTTCTGAGG 409
DB 315 GTACGCTGACACTGTGAGTGGCTGACCTCTCTTGTGATCAGACCTCCCTTCTGAGG 374
QY 410 AGTTGATGTCAGTGTGAGTGTGATGAGGTTTACAGAGAAGCTAAGAGCATGACGAGCAA 469
DB 375 AGTTGATGTCAGTGTGAGTGTGATGAGGTTTACAGAGAAGCTAAGAGCATGACGAGCAA 434
QY 470 CTACAGTCTCAACCTCTACAGAGGCTTCTATCTGCTTCACTACCTGAGAGAGGTA 529
DB 435 CTACAGTCTCAACCTCTACAGAGGCTTCTATCTGCTTCACTACCTGAGAGAGGTA 494
QY 530 CCTGCGCATTTGTCCAGCGCCACCAAGTCAAGAGGCAAGAACTGCTGAGTGAAGAGG 589
DB 495 CTTGCGCATTTGTCCAGCGCCACCAAGTCAAGAGGCAAGAACTGCTGAGTGAAGAGG 554
QY 590 AGTATATGTTGGGCTGTGATGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 649
DB 555 GGTATATGTTGGGCTGTGATGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 614
QY 650 CGAGCTCAGCCAGGGGAGCATCAGTCAAGGGGATGAGTCAATCTGAGAGCGCTTGA 709
DB 615 CAAG-----TCAGTGAAGGAGATGAGTCAATCTGAGAGCGCTTGA 659
QY 710 CCGGATGAGCTGTGATGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 769

230 TTTCATAGAGATCTTCCTGGCCACCATCTTATCATCTCTTGACGTGGCATAGTCG 289
195 TTTCATATAATATCTTCCTGGCCACCATCTTATCATCTCTTGACGTGGCATAGTCG 254
290 CAATGATATGATATCTTCCTGGCCACCATCTTATCATCTCTTGACGTGGCATAGTCG 349
255 CAATGATATGATATCTTCCTGGCCACCATCTTATCATCTCTTGACGTGGCATAGTCG 314
350 GTACCGCTGACCTGTCATCTGCTGACCTCTCTTGTATCATCTACACTCCCTCTGCGC 409
315 GTACAGGCTGACCTGTCATCTGCTGACCTCTCTTGTATCATCTACACTCCCTCTGCGC 374
410 AGTTGATGCTGACCTGTCATCTGCTGACCTCTCTTGTATCATCTACACTCCCTCTGCGC 469
375 AGTTGATGCTGACCTGTCATCTGCTGACCTCTCTTGTATCATCTACACTCCCTCTGCGC 434
470 CTACATGTCATACCTTACAGCAGCAGCTTCTATCTGCTGACCTCTTGTATCATCTACACT 529
435 CTACATGTCATACCTTACAGCAGCAGCTTCTATCTGCTGACCTCTTGTATCATCTACACT 494
530 CTTCGCTATGTCACGCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCT 589
495 CTTCGCTATGTCACGCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCT 554
590 AGTTGATGCTGACCTGTCATCTGCTGACCTCTCTTGTATCATCTACACTCCCTCTGCGC 649
555 AGTTGATGCTGACCTGTCATCTGCTGACCTCTCTTGTATCATCTACACTCCCTCTGCGC 614
650 CGAGTCAGCAGCAGGCGGACATCACTGACGCGGATGACAGTACATCTGTCACCTCTTGA 709
615 CAAGC-----TCAGTGAAGGAGATGACAGATATCTGTCAGCCTCTCTA 659
710 CCCGATAGCTGTCATCTGCTGACCTCTCTTGTATCATCTACACTCTTGTATCATCT 769
660 CCCGATAGCTGTCATCTGCTGACCTCTCTTGTATCATCTACACTCTTGTATCATCT 719
770 GCGCGGATGTCATCTGCTGACCTCTCTTGTATCATCTACACTCTTGTATCATCT 829
720 GCGCGGATGTCATCTGCTGACCTCTCTTGTATCATCTACACTCTTGTATCATCT 779
830 GCGCGGATGTCATCTGCTGACCTCTCTTGTATCATCTACACTCTTGTATCATCT 889
780 GCGCGGATGTCATCTGCTGACCTCTCTTGTATCATCTACACTCTTGTATCATCT 839
890 CTGCTGCTGTCATCTGCTGACCTCTCTTGTATCATCTACACTCTTGTATCATCT 949
840 CTGCTGCTGTCATCTGCTGACCTCTCTTGTATCATCTACACTCTTGTATCATCT 899
950 CAAGCAGATGTCATCTGCTGACCTCTCTTGTATCATCTACACTCTTGTATCATCT 1009
900 CAAGCAGATGTCATCTGCTGACCTCTCTTGTATCATCTACACTCTTGTATCATCT 959
1010 CGGCTGCTGTCATCTGCTGACCTCTCTTGTATCATCTACACTCTTGTATCATCT 1069
960 AGTTGATGCTGACCTGTCATCTGCTGACCTCTCTTGTATCATCTACACTCTTGTAT 1019
1070 AGTTGATGCTGACCTGTCATCTGCTGACCTCTCTTGTATCATCTACACTCTTGTAT 1129
1020 AAGCTGCTGACCTGTCATCTGCTGACCTCTCTTGTATCATCTACACTCTTGTAT 1079
1130 CAAGCAGATGTCATCTGCTGACCTCTCTTGTATCATCTACACTCTTGTATCATCT 1139
1080 CAAGCAGATGTCATCTGCTGACCTCTCTTGTATCATCTACACTCTTGTATCATCT 1139
1190 CTGCTGCTGTCATCTGCTGACCTCTCTTGTATCATCTACACTCTTGTATCATCT 1249
1140 CTGCTGCTGTCATCTGCTGACCTCTCTTGTATCATCTACACTCTTGTATCATCT 1191
1250 TTTCATAGAGATCTTCCTGGCCACCATCTTATCATCTCTTGACGTGGCATAGTCG 1309
1192 TTTCATAGAGATCTTCCTGGCCACCATCTTATCATCTCTTGACGTGGCATAGTCG 1251

1310 TTTCATAGAGATCTTCCTGGCCACCATCTTATCATCTCTTGACGTGGCATAGTCG 1369
1252 TTTCATAGAGATCTTCCTGGCCACCATCTTATCATCTCTTGACGTGGCATAGTCG 1305
1370 ATATGATATGATATCTTCCTGGCCACCATCTTATCATCTCTTGACGTGGCATAGTCG 1429
1306 TTTCATAGAGATCTTCCTGGCCACCATCTTATCATCTCTTGACGTGGCATAGTCG 1361
1430 AGTTGATGCTGACCTGTCATCTGCTGACCTCTCTTGTATCATCTACACTCCCTCTGCGC 1489
1362 AGTTGATGCTGACCTGTCATCTGCTGACCTCTCTTGTATCATCTACACTCCCTCTGCGC 1413
1490 ACATTCAGATGTCATCTGCTGACCTCTCTTGTATCATCTACACTCCCTCTGCGC 1549
1414 ACATTCAGATGTCATCTGCTGACCTCTCTTGTATCATCTACACTCCCTCTGCGC 1473
1550 ATATGATATGATATCTTCCTGGCCACCATCTTATCATCTCTTGACGTGGCATAGTCG 1609
1474 TAGATATGATATCTTCCTGGCCACCATCTTATCATCTCTTGACGTGGCATAGTCG 1488
1610 AGTTGATGCTGACCTGTCATCTGCTGACCTCTCTTGTATCATCTACACTCCCTCTGCGC 1669
1489 AGTTGATGCTGACCTGTCATCTGCTGACCTCTCTTGTATCATCTACACTCCCTCTGCGC 1525
1670 TTTCATAGAGATCTTCCTGGCCACCATCTTATCATCTCTTGACGTGGCATAGTCG 1729
1526 TTTCATAGAGATCTTCCTGGCCACCATCTTATCATCTCTTGACGTGGCATAGTCG 1581
1730 TTTCATAGAGATCTTCCTGGCCACCATCTTATCATCTCTTGACGTGGCATAGTCG 1789
1582 TTTCATAGAGATCTTCCTGGCCACCATCTTATCATCTCTTGACGTGGCATAGTCG 1623
1790 GTACAGCTGTCATCTGCTGACCTCTCTTGTATCATCTACACTCTTGTATCATCT 1849
1624 GTACAGCTGTCATCTGCTGACCTCTCTTGTATCATCTACACTCTTGTATCATCT 1683
1850 AAAAAAAAAAAAAAAAAAAAAAAAAA 1877
1684 AAAAAAAAAAAAAAAAAAAAAAAAAA 1711

RESULT 6
US-08-802-627A-3
Sequence 3, Application US/08802627A
Patent No. 5892017
GENERAL INFORMATION:
APPLICANT: Lee, James
TITLE OF INVENTION: NUCLEIC ACID ENCODING P4A RECEPTOR
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/802.627A
FILING DATE: 19-Feb-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/284586
FILING DATE: 10-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/076093
FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA:


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      840 CTGTGGCTGCTTACTTACTATGATGGATCGACATCGACTCTTCTATCTCTCTGGAATCAT 899
      950 CAAGCAAGATGATGACTTGGAGACATGTGACAGCATGTGATGATCTCATCAAGAGCCCT 1009
      900 CAAAGCAAGGTGTGATTTGAGACACTGTGCAAAAGTGTGATTTCCATCAAGAGCCCT 959
      1010 CGGCTTCTTCACTGTGTGCTGAACCCATCCCTCTGTGCTTCTGCGGGCCAAAGTTCAA 1069
      960 AGCTTTCTTCACTGTGTGTGTAACCCCATCCCTCTGTGCTTCTGAGCCAAATTTAA 1019
      1070 AAGCTTCCCGACAGATGACATCACTCATGAGCAGAGGCTCCAGCTCAAGATCTTTC 1129
      1020 AACTCTGCCCGACAGCAGCATCTCTGTGAGCAGAGGCTCCAGCTCAAGATCTCTTC 1079
      1130 CAAAGCAAGCGGGGTGAGACATCTTCCGCTCCAGAGGATGAGATCTCTCCAGTTTCA 1189
      1080 CAAAGCAAGCGGGGTGAGACATCTTCCGCTCCAGAGGATGAGATCTCTCCAGTTTCA 1139
      1190 CTCACACTAACCTTATGCAAGACTTATATATATATATATATATATATATATATATAT 1249
      1140 CTCACACTAA-----CACAGATGTAAAGACTTTTATATATATATATATATATATAT 1191
      1250 TTTTATGTTACACATTTTCCAGATATTAAGAGACTGACAGCTTGTACAGTTTTTTT 1309
      1192 TTTTAAAGTTACATTTTTCAGATATATAAAGACTGACCAATATTTGACAGTTTTTATGC 1251
      1310 TTTTAAATGACGTGGGAGTTTATGTCCTTACTATTTTGTGAGAGTTGACTTATTT 1369
      1252 TTGTGGATTTTTTGT-----CTTGTGTTCTTTTATTTTGTGAAGTTAATGTACT 1305
      1370 ATATAAATATGTTTGTGTTTGTTCATGATGATGATGAGCTGAGCAGAGACTGTGGCC 1429
      1306 TTTATA-----TAAATTTTTTGTGTTTGTTCATATGATGATGATGAGCAGAGACTGTGGCC 1361
      1430 AAGTCTTGTGATGCTTTATCTGTGTGAGAGACTGATAGACTGTGAGAGAGAACTGA 1489
      1362 AAGTCTTGTGATGCTTTATCTGTGTGAGAGACTGATAGAA-----AAGGAGACTGA 1413
      1490 ACATTCACAAGTGTGTAATTAATTAAGATAGCCGTGATGATGATGATGATGATGATG 1549
      1414 ACATTCACAAGTGTGTAATTAATTAAGATAGCCGTGATGATGATGATGATGATGATG 1473
      1550 TAATCTCTTCAATCCAGAGAGACCCACCCACCCACCCACCCACCCACCATTTCTAAT 1609
      1474 TAGATTAATCTTCCA----- 1488
      1610 TGTGGTGAATGCTGTGATAGGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTT 1669
      1489 -----TTCCCGTGAAGCTTTTCTGTTCTGTTCTTAAGACGTGAT 1525
      1670 TTTTCTGTAAGATGACACTTAACCAAGCCTTAATGTGGGTGAGAAATCTGTGGGT 1729
      1526 TTTGCTGTGAAGATGACACTTAACCAAGCCTTAATGTGGGTGAGAAATCTGTGGGT 1581
      1730 TTTTGTGTTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTT 1789
      1582 -----TTTTCAGTTTTCAGAGAGGAGGTTGATTTTCAGACACTTAC-AGT 1623
      1790 GTACACTCTGTGATTAATCAATGTTAATTAAGATCAATGATTAATTAATTAATTAAT 1849
      1624 GTACACTCTGTGATTAATCAATGTTAATTAAGATCAATGATTAATTAATTAATTAAT 1683
      1850 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1877
      1684 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1711

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RESULT 9
 US-09-104-296-3
 ; Sequence 3, Application US/09104296
 ; Patent No. 6087475
 ; GENERAL INFORMATION:

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      ? APPLICANT: Lee, James
      ? APPLICANT: Wood, William I.
      ? TITLE OF INVENTION: PF4A Receptors
      ? NUMBER OF SEQUENCES: 6
      ? CORRESPONDENCE ADDRESS:
      ? ADDRESSEE: Genentech, Inc.
      ? STREET: 1 DNA Way
      ? CITY: South San Francisco
      ? STATE: California
      ? COUNTRY: USA
      ? ZIP: 94080
      ? COMPUTER READABLE FORM:
      ? MEDIUM TYPE: 3.5 Inch, 1.44 Mb floppy disk
      ? COMPUTER: IBM PC compatible
      ? OPERATING SYSTEM: PC-DOS/MS-DOS
      ? SOFTWARE: Winpatin (Genentech)
      ? CURRENT APPLICATION DATA:
      ? APPLICATION NUMBER: US/09/104,296
      ? FILING DATE: 24-June-1998
      ? CLASSIFICATION:
      ? PRIOR APPLICATION DATA:
      ? APPLICATION NUMBER: 08/701265
      ? FILING DATE: 22-AUG-1996
      ? PRIOR APPLICATION DATA:
      ? APPLICATION NUMBER: 08/664228
      ? FILING DATE: 06-JUN-1996
      ? PRIOR APPLICATION DATA:
      ? APPLICATION NUMBER: 08/076093
      ? FILING DATE: 11-JUN-1993
      ? PRIOR APPLICATION DATA:
      ? APPLICATION NUMBER: 07/810782
      ? FILING DATE: 19-DEC-1991
      ? ATTORNEY/AGENT INFORMATION:
      ? NAME: Love, Richard B.
      ? REGISTRATION NUMBER: 34,659
      ? REFERENCE/DOCKET NUMBER: P07062C2
      ? TELECOMMUNICATION INFORMATION:
      ? TELEPHONE: 415/225-5530
      ? TELEFAX: 415/952-9881
      ? TELEX: 910/371-7168
      ? INFORMATION FOR SEQ ID NO: 3:
      ? SEQUENCE CHARACTERISTICS:
      ? LENGTH: 1737 base pairs
      ? TYPE: Nucleic Acid
      ? STRANDEDNESS: Single
      ? TOPOLOGY: Linear
      ? US-09-104-296-3
      ?
      Query Match      51.9%; Score 974.4; DB 3; Length 1737;
      Best Local Similarity 76.1%; Pred. No. 2.1e-187;
      Matches 1391; Conservative 0; Mismatches 301; Indels 136; Gaps 10;
      ?
      QY      50 GCAGGTAGCAGTGAACCTCTGAGGCGTTGGTCTCCGTTAAACACACGAGGCTGAGAC 109
      DB      20 GCGCGGCGCAAGTGAAGCGGCGGCTGAGTCTCCAGTAGCCAGCGATCTGGAGAAC 79
      ?
      QY      110 GAGGTGTCAGTGAACCATCAGTGTGATATATACCTTCTGATTAATCTGTAAGA 169
      DB      80 CAGCGGTACCATGGA-----GGGATCAGTATATACCTTTCAGATTAATCAACGAGGA 134
      ?
      QY      170 AGTGGGCTGAGAGATATGACTCCACAAGAACCTCTTCCGGGATGAAAGCTGCA 229
      DB      135 AATGGGCTCAGGGGACTATGACTCCATGAAGAACCTCTTTCGGGAGAAATGCTGA 194
      ?
      QY      230 TTTCATTAAGATCTTCTGCCCCACATCTACTTCAATCTTCTGACTGGGATGCTG 289
      DB      195 TTTCATTAAGATCTTCTGCCCCACATCTACTTCAATCTTCTTAACTGATGCTGGG 254
      ?
      QY      290 CAATGATGTGATGATCTGCTGATGATGATGATGATGATGATGATGATGATGATGATG 349
      DB      255 CAATGATGTGATGATCTGCTGATGATGATGATGATGATGATGATGATGATGATGATG 314
      ?
      QY      350 GTACCGGTGACACTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 409

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Db 315 GTACAGGCTGCACCTGTCAGTGGCCGACCTCTTGTGTCATCAGCTTCCCTTGCGGC 374
QY 410 AGTGAATGCCATGGCTGACGTGACTTTGGGAAATTTTGTGTAAGCTTCCATATCAT 469
Db 375 AGTTGATGCCGTGGCAAACTGTGACTTTGGGAACTTCTTAAGCAAGCACTCCATGTGCA 434
QY 470 CTACACTGTCACCTGTACAGCAGCTTCATCTGCGCTTCATGAGCTTGAGCGGTA 529
Db 435 CTACACAGTCAACCTGTACAGAGTGTCCATCTCGGCTTCATGAGTGTGAGCCGCTA 494
QY 530 CTTGCCATTTGTCCAGGCCACCAACAGTCAAGGCCAAGAACTGCTGCTGAAAAGC 569
Db 495 CCGGCGATCTGTCAGCGCCACCAACAGTCAAGGCCAAGAACTGCTGCTGAAAAGT 554
QY 590 AGTCTATGTGGGGTGGATGCCAGCCCTCTCGACTATACCTGACTTCATCTTTGCG 649
Db 555 GGTCTATGTGGGTGGATGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 614
QY 650 CGACGTACAGCCAGGGGACATCAGTACAGGGGATGACAGTACATCTGACCCGCTTA 709
Db 615 CAACG-----TCAGTACAGATGACAGATATATCTGTGACCGCTTCTA 659
QY 710 CCCCAGTACCTGTGATGCTGCTTTCATTCAGCATATATAGTGGTCTGATCT 769
Db 660 CCCCAGTACCTGTGATGCTGCTTTCATTCAGCATATATAGTGGTCTGATCT 719
QY 770 GCGCGCATGCTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 829
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QY 830 GGGCCACAGAACGCGAGGCTCTCAAGACAGTATCTGATCTGCTGCTGCT 889
Db 780 GGGCCACAGAACGCGAGGCTCTCAAGACAGTATCTGATCTGCTGCTGCTGCT 839
QY 890 CTGCTGGCTGCCATATATATGTTGGGATCAGATCAGTCTCTTATCTTTGGAGTCA 949
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QY 950 CAAGCAAGATGTGACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1009
Db 900 CAAGCAAGATGTGACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 959
QY 1010 CCGCTTCTTCACTGTTGCTGACCCCATCTCTATGCTTCTGCGGCGCAAGTCA 1069
Db 960 AGCTTCTTCACTGTTGCTGACCCCATCTCTATGCTTCTGCGGCGCAAGTCA 1019
QY 1070 AAGCTTCTGCGCAGATGCTCAACTGATGACAGAGGCTCCAGCTCAAGTCTTTC 1129
Db 1020 AAGCTTCTGCGCAGATGCTCAACTGATGACAGAGGCTCCAGCTCAAGTCTTTC 1079
QY 1130 CAAGGAAAGCGGGGAGACATCTTCCGTCACAGAGTGAAGATCCCGCTTTC 1189
Db 1080 CAAGGAAAGCGGGGAGACATCTTCCGTCACAGAGTGAAGATCCCGCTTTC 1139
QY 1190 CTGCACTAACCTTATGCAAGACTTATATATATATATATATATATATATAT 1249
Db 1140 CTGCACTAACCTTATGCAAGACTTATATATATATATATATATATATATAT 1191
QY 1250 TTTTATGTTACATTTTCCAGATATAGAGACTGACCACTGTTACAGTCTTTT 1309
Db 1192 TTTTATGTTACATTTTCCAGATATATATATATATATATATATATATAT 1251
QY 1310 TTTTATGTTACATTTTCCAGATATAGAGACTGACCACTGTTACAGTCTTT 1369
Db 1252 TTTTATGTTACATTTTCCAGATATAGAGACTGACCACTGTTACAGTCTTT 1305
QY 1370 ATATATAATATTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1429
Db 1306 TTTTATA-----TAATTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1361
QY 1430 AAGTCTTACAGCTGTTATCTGCTGTAAGAGCTGACAGTGTGAGAGAACTGA 1489

Db 1362 AAGTCTTACAGCTGTTATCTGCTGTAAGAGCTGTAAGAA-----AAGGAAGTGA 1413
QY 1490 ACATTCAGAGTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1549
Db 1414 ACATTCAGAGTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1473
QY 1550 TAATCTCTTCAATTCAGAGAGGACCCACCACCACCACCACCACCACCACCATTCTTAAT 1609
Db 1474 TAGATATCTCTCA----- 1488
QY 1610 TGTGTTGTTATGCTGTGATGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1669
Db 1489 -----TTCCCGGAGAACCTTTTCTGTTCTGTTACAGCTGAT 1525
QY 1670 TTTTCTGTAAGAGTGCACCTTAACCAAGCTCAATGTTGTTGTTGTTGTTGTT 1729
Db 1526 TTTGCTGTGTAAGATGCTGCTTATACCAAGCCCAAGTGT-ATAGAAATGCTGG- 1581
QY 1730 TTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1789
Db 1582 -----TTTTCAGTTTCAGAGAGTGGGTGATTTTCAGACCTTAC-AGT 1623
QY 1790 GTACAGTCTGTTATTCATTTGTTAATAAAGTCAATGATTAATTAATAAATAA 1849
Db 1624 GTACAGTCTGTTATTCATTTGTTAATAAAGTCAATGATTAATTAATAAATAA 1683
QY 1850 AAAAAAAAAAAAAAAAAAAAAAAAAA 1877
Db 1684 AAAAAAAAAAAAAAAAAAAAAAAAAA 1711

RESULT 10
PCT-US94-06380-2
; Sequence 2, Application PC/TUS9406380
; GENERAL INFORMATION:
; APPLICANT: Chundharapal, Anan
; APPLICANT: Lee, James
; APPLICANT: Hebert, Caroline
; APPLICANT: K. Jin Kim
; APPLICANT: Genentech, Inc.
; TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY DISORDERS
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/06380
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/076093
; FILING DATE: 11-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: 706F2P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ. ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1737 bases
; TYPE: nucleic acid

OY	45	AGGTGGCAGGTAGGAGAGACCTCTGTGAGGGCTTTGGTGTCCGGTAACACCAAGGGCT	104
Db	1	CGGCACGAGGTAGCAAAAGTAGACCGCAGGGCTTAGTGTCTCAGTAGCCAGCATCTGG	60
OY	105	AGACGAGTGTGGCCATGGAACCGCATAGTGTGAGTATATACACTTGTGATTAACACTCT	164
Db	61	AGAACCGAGGTTACCATGGA-----GGGATTCAGTATATACACTTCCAGTAACTACACC	115
OY	165	GAAAGAGTGGGGTGTGGAGACTATGACTCCAACAGAAAGAACCTCTTCGGGGATGAAAC	224
Db	116	GAGGAAATGGGCTCAGGGAGCTATGACTCCATGGAAGAACCTCTTCCGGAAGAAAT	175
OY	225	GTCATTTCATAGGATCTTCTGCGCCACCATCTACTTCATCATCTCTTGACGGGATA	284
Db	176	GCTATTTCATTAATAATCTTCTCTGCCACCATCTACTTCATCATCTCTTAAGCGCAT	235
OY	285	GTCGGCAATGAGATTGTGTGATCCTGGTCATGGGTTACAGAAAGCTAAGGAGCATGACG	344
Db	236	GTGGGCAATGAGATTGTGTATCCTGGTATAGGTTATCCAGAAAGAACTGAAAGCATGACG	295
OY	345	GACAAATACCGGGCTGCACCTGTCAGTGGCTAACCCTCTTGTGATCACACTCCCTTC	404
Db	296	GACAAGTACAGGCTGCACCTGTCAGTGGCCGACACTCCTTGTGATCACACTCCCTTC	355
OY	405	TGGGAGTGAATGCAATGGCTGACGTGACGTGACTTTGGGAAATTTGTGTAAGCGTGCAT	464
Db	356	TGGGAGTGAATGCGGTGGCAAACTGGGACTTTGGGAACTTCTATGCAAGGCAATCAT	415
OY	465	ATCATCTACATGTCAACCTCTACAGCAGCCTTTCATCTCGGCCTCATGAGCTGGAC	524
Db	416	GTCAATCTACAGATCAACCTCTACAGCAGTGTCTCATCTCGGCCTCATGAGCTGGAC	475
OY	525	CGGTACCTGCCATTTGTCACGCGCACCAACAGTCAAAAGGCCAAGAAACTGTGGCTGAA	584
Db	476	CGTACCTGGGCATCTGTCCACGCGCACCAACAGTCAAGGCCAAGAAACTGTGGCTGAA	535
OY	585	AAGGAGCTATMGGGGGGCTGTGATGCCACCCCTCTCTGACTATACCTGACTTCATC	644
Db	536	AAGGAGCTATMGGGGGGCTGTGATGCCCTCTCTCTGACTATACCTGACTTCATC	595
OY	645	TTTGGCAGCTACGACGAGGGGAGACATCAGTGAAGGGGATGACAGGTACATGTGACCGC	704
Db	596	TTTGGCAGC-----TCAGTGAAGGAGATGACAGATATATCTGTGACCGC	640
OY	705	CTTACCCCGATAGCCTGTGATGGTGTGTTTCAATTCAGACATATATATGATGGGTCTC	764
Db	641	TTTACCCCGATAGCCTGTGATGGTGTGTTTCAAGTTTCAGACATATATGATGGGTCTT	700
OY	765	ATCTGCCCGGCGATCTGATCTCTCTCTGTATCTGATCATCATCTCTAAGCTGTACAC	824
Db	701	ATCTGCCCTGATTTGATCTCTCTCTCTGCTATTTGATTCATTCATCTCCMACCTGTACAC	760
OY	825	TCGAAGGGCACACGAAGCGCAAGGCCCTCAAGAGAGACATCATCTCATGCTTACGCTTC	884
Db	761	TCGAAGGGCACACGAAGCGCAAGGCCCTCAAGAGACATCATCTCATGCTTACGCTTTC	820
OY	885	TTTGGCTGCTGAGCTCCATATTTATGTGGGATTCAGACATGCACTCCTTCATCTTTGGGA	944
Db	821	TTTGGCTGCTGAGCTCCTTACTACATTTGGGATTCAGACATGCACTCCTTCATCTCCTGGAA	880
OY	945	GTCATCAAGCAAGATGTGACTTGCAGAGCATTTGTGCAACAAGTGGATTCATCAACAG	1004
Db	881	ATCATCAAGCAAGAGGTGTGAGTTTGGAACTGTGCACAAGTGGATTTCCATCACCGAG	940
OY	1005	GCCCTGAGCTTCTTACACTGTGTGCTGAAACCCATCTTATGCTTCTGTGGGGCCAG	1064
Db	941	GCCCTGAGCTTCTTCCACTGTTGTGTGAACCCCATCTTATGCTTCTTGTGAACCCAAA	1000
OY	1065	TTCAAAAGCTCTGCCACATGACATCAACTCATGAGCAGAGGCTCCAGCTCAAGATC	1124
Db	1001	TTTAAAGCTCTGCCACAGCACTCATCTGTGTGAGCAGAGGCTCCAGCTCAAGATC	1064
OY	1125	CTTTCAAAAGGAAGCGGGGTGAGACACTTTCCTCTTCACAGAGTCAGAATCTCCAGT	1184

[illegible]

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1 RESULT 13
2 US-08-153-848-45
3 Sequence 45, Application US/08153848
4 Patent No. 5759804
5 GENERAL INFORMATION:
6 APPLICANT: Godiska, Ronald
7 APPLICANT: Gray, Patrick W.
8 APPLICANT: Schweikart, Vicki L.
9 TITLE OF INVENTION: No. 5759804el Seven Transmembrane Receptors
10 NUMBER OF SEQUENCES: 64
11 CORRESPONDENCE ADDRESSES:
12 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
13 ADDRESSEE: Bicknell
14 STREET: 6300 Sears Tower, 233 South Wacker Drive
15 CITY: Chicago
16 STATE: Illinois
17 COUNTRY: USA
18 ZIP: 60606
19 COMPUTER READABLE FORM:
20 MEDIUM TYPE: Floppy disk
21 COMPUTER: IBM PC compatible
22 OPERATING SYSTEM: PC-DOS/MS-DOS
23 SOFTWARE: Patentln Release #1.0, Version #1.25
24 CURRENT APPLICATION DATA:
25 APPLICATION NUMBER: US/08/153,848
26 FILING DATE:
27 CLASSIFICATION: 514
28 PRIOR APPLICATION DATA:
29 APPLICATION NUMBER: US 07/977,452
30 FILING DATE: 17-NOV-1992
31 ATTORNEY/AGENT INFORMATION:
32 NAME: No. 5759804and, Greta E.
33 REGISTRATION NUMBER: 35,302
34 REFERENCE/DOCKET NUMBER: 31794
35 TELECOMMUNICATION INFORMATION:
36 TELEPHONE: (312) 474-6300
37 TELEFAX: (312) 474-0448
38 TELEX: 25-3856
39 INFORMATION FOR SEQ ID NO: 45:
40 SEQUENCE CHARACTERISTICS:
41 LENGTH: 1317 base pairs

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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 201..1211
US-08-153-848-45

Query Match 44.5%; Score 834.6; DB: 1; Length 1317;
Best Local Similarity 83.9%; Pred. No. 2.6e-159;
Matches 977; Conservative 0; Mismatches 164; Indels 24; Gaps 2;

QY 134 TGTGAGTATATACCTTCTGTAGTACTCTGGAAGAGTGGGTCTGAGAGTATGACTC 193
DB 164 TTTGAGATATACCTTCTGTAGTACTCTGGAAGAGTGGGTCTGAGAGTATGACTC 223
QY 194 CAACAGAGACCCCTGCTTCCGGGATGAAACGTCATTTCAATAGATCTTCCGCCAC 253
DB 224 CATGAGAGAACCCCTGCTTCCGGGATGAAACGTCATTTCAATAGATCTTCCGCCAC 283
QY 254 CATCTACTCTCATCTCTCTGAGTACTGTCATGTCGCAATGGATTGGTATCCTGTCAT 313
DB 284 CATCTACTCTCATCTCTCTGAGTACTGTCATGTCGCAATGGATTGGTATCCTGTCAT 343
QY 314 GGGTTACAGAGAAGCTAAGAGCATGACGACAGACAGTACCGGCTGCACTGTGAGTGC 373
DB 344 GGGTTACAGAGAAGCTAAGAGCATGACGACAGACAGTACCGGCTGCACTGTGAGTGC 403
QY 374 TGACCTCTCTTTGTATCATACATCCCTCTGCGGCACTGTGATCCATGCTGATGTA 433
DB 404 CGACCTCTCTTTGTATCATACATCCCTCTGCGGCACTGTGATCCATGCTGATGTA 463
QY 434 CTTTGGGAATTTTGTGTAGGCTGTGTCATATCATCTACATCACTGTCACACCTCTACAGAG 493
DB 464 CTTTGGGAATTTTGTGTAGGCTGTGTCATATCATCTACATCACTGTCACACCTCTACAGAG 523
QY 494 CGTTCTCATCTCTGCTTCTCATACCTGACCGGCTGACCTGCACTTGTCCAGCCACCAA 553
DB 524 TGTCTCTATCTCTGCTTCTCATACCTGACCGGCTGACCTGCACTTGTCCAGCCACCAA 583
QY 554 CAGTCAAGGCGCAAGAGAACTGCTGCTGAAAGAGCACTATATGTTGGGCTGTGATGCC 613
DB 584 CAGTCAAGGCGCAAGAGAACTGCTGCTGAAAGAGCACTATATGTTGGGCTGTGATGCC 643
QY 614 AGCCCTCTCTGCTGCTTCTCATACCTGACCGGCTGACCGGCTGCACTTGTCCAGCCACCAA 673
DB 644 TGCCTCTCTGCTGCTTCTCATACCTGACCGGCTGACCGGCTGCACTTGTCCAGCCACCAA 688
QY 674 TCAGGGGAGATGACAGATATCTGTGACCGGCTTACCCGATAGCCTGTGATGCTGCT 733
DB 689 TGAGGCAAGATGACAGATATCTGTGACCGGCTTACCCGATAGCCTGTGATGCTGCT 748
QY 734 GTTTCATTTCCAGATATATGTTGGGCTGTATCTGCGGCACTGCTATCTCTCTCTG 793
DB 749 GTTTCATTTCCAGATATATGTTGGGCTGTATCTGCGGCACTGCTATCTCTCTCTG 808
QY 794 TTACTGATCATCTCTGATGCTGTGACCTGCACTGCAAGGCGCAGAGGCGCT 853
DB 809 CTATTGATTTATCTCTGATGCTGTGACCTGCACTGCAAGGCGCAGAGGCGCT 868
QY 854 CAAGAGCAGATCTCTGATGCTGTGACCTGCACTGCAAGGCGCAGAGGCGCT 913
DB 869 CAAGAGCAGATCTCTGATGCTGTGACCTGCACTGCAAGGCGCAGAGGCGCT 928
QY 914 GATGAGCATGATCTCTGATGCTGTGACCTGCACTGCAAGGCGCAGAGGCGCT 973
DB 929 GATGAGCATGATCTCTGATGCTGTGACCTGCACTGCAAGGCGCAGAGGCGCT 988
QY 974 CATGTGCAAGAGGATCTCTGATGCTGTGACCTGCACTGCAAGGCGCAGAGGCGCT 1033
DB 989 CATGTGCAAGAGGATCTCTGATGCTGTGACCTGCACTGCAAGGCGCAGAGGCGCT 1048

QY 1034 CCCCATCTCTATGCTCTCTGCGGCGCAAGTTCACAAAGCTCTGCCAGCATGCTCAA 1093
DB 1049 CCCCATCTCTATGCTCTCTGCGGCGCAAGTTCACAAAGCTCTGCCAGCATGCTCAA 1108
QY 1094 CTCCATGAGCAGAGGCTCTCCAGCTCTCAAGATCTTTTCAAGAGAAAGCGGGGTGACACTC 1153
DB 1109 CTCTGTGAGCAGAGGCTCTCCAGCTCTCAAGATCTTTTCAAGAGAAAGCGGGGTGACACTC 1168
QY 1154 TTCCGCTCTCCAGGAGTCAAGATCTCCAGTCTTCACTCCAGCTTATCCAGTCAAGA 1213
DB 1169 ATCTGTTCCAGTCAAGTCTCTCAAGTCTTCACTCCAGCTTATCCAGTCAAGA 1226
QY 1214 CTTAT 1273
DB 1227 -----AGACTTTTAT 1279
QY 1274 ATAGAGACTGACCACTCTGTACA 1298
DB 1280 ATAGAGACTGACCACTGTGTGAAA 1304

RESULT 14

US-09-299-843A-45
Sequence 45, Application US/09299843A
Patent No. 6107475

GENERAL INFORMATION:
APPLICANT: Godiska, Ronald

APPLICANT: Gray, Patrick W.

APPLICANT: Schwaikart, Vicki L.

TITLE OF INVENTION: No. 6107475e1 Seven Transmembrane Receptors

NUMBER OF SEQUENCES: 66

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &

STREET: 6300 Sears Tower, 233 South Wacker Drive

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/299,843A

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/088,337

FILING DATE: 01-JUN-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/153,848

FILING DATE: 17-NOV-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/977,452

FILING DATE: 17-NOV-1992

ATTORNEY/AGENT INFORMATION:

NAME: JILL E. Uhl

REGISTRATION NUMBER: 43,213

REFERENCE/DOCKET NUMBER: 27866/32059B

TELECOMMUNICATION INFORMATION:

TELEPHONE: (312) 474-6300

TELEFAX: (312) 474-0448

TELEX:

INFORMATION FOR SEQ ID NO: 45:

SEQUENCE CHARACTERISTICS:

LENGTH: 1317 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

FEATURE:

NAME/KEY: CDS
LOCATION: 201..1211
US-09-299-843A-45

Query Match 44.5%; Score 834.6; DB 3; Length 1317;
Best Local Similarity 83.9%; Pred. No. 2.6e-159;
Matches 977; Conservative 0; Mismatches 164; Indels 24; Gaps 2;

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164 TTTCAGATATATACACTTGTATACACTCTGTGAGAGAGTGGGCTGAGACATGATGACTC 223
194 CAAGAAGAACTCTGTGAGAGAGTGGGCTGAGACATGATGACTC 253
224 CATGAAGAACTCTGTGAGAGAGTGGGCTGAGACATGATGACTC 283
254 CATCTACTCTGTGAGAGAGTGGGCTGAGACATGATGACTC 313
284 CATCTACTCTGTGAGAGAGTGGGCTGAGACATGATGACTC 343
314 GGGTACAGAGAGAGTGGGCTGAGAGAGTGGGCTGAGAGAGTGGGCTGAGAGAGTGGGCT 373
344 GGGTACAGAGAGAGTGGGCTGAGAGAGTGGGCTGAGAGAGTGGGCTGAGAGAGTGGGCT 403
374 TGACCTCTCTGTGAGAGAGTGGGCTGAGAGAGTGGGCTGAGAGAGTGGGCTGAGAGAGT 433
404 CGACCTCTCTGTGAGAGAGTGGGCTGAGAGAGTGGGCTGAGAGAGTGGGCTGAGAGAGT 463
434 CTCTGGGAAATTTTGTGAGAGAGTGGGCTGAGAGAGTGGGCTGAGAGAGTGGGCTGAGAG 493
464 CTCTGGGAAATTTTGTGAGAGAGTGGGCTGAGAGAGTGGGCTGAGAGAGTGGGCTGAGAG 523
494 CGTCTCTCTGTGAGAGAGTGGGCTGAGAGAGTGGGCTGAGAGAGTGGGCTGAGAGAGTGGG 553
524 TGCTCTCTGTGAGAGAGTGGGCTGAGAGAGTGGGCTGAGAGAGTGGGCTGAGAGAGTGGG 583
554 CAGTCAAGAGAGAGTGGGCTGAGAGAGTGGGCTGAGAGAGTGGGCTGAGAGAGTGGGCTG 613
584 CAGTCAAGAGAGAGTGGGCTGAGAGAGTGGGCTGAGAGAGTGGGCTGAGAGAGTGGGCTG 643
614 AGGCTCTCTGTGAGAGAGTGGGCTGAGAGAGTGGGCTGAGAGAGTGGGCTGAGAGAGTGG 673
644 TGCTCTCTGTGAGAGAGTGGGCTGAGAGAGTGGGCTGAGAGAGTGGGCTGAGAGAGTGGG 693
674 TCAGAGAGAGAGTGGGCTGAGAGAGTGGGCTGAGAGAGTGGGCTGAGAGAGTGGGCTGAG 723
689 TGAGAGAGAGAGTGGGCTGAGAGAGTGGGCTGAGAGAGTGGGCTGAGAGAGTGGGCTGAG 748
734 GTTCAATTCAGAT 793
749 GTTCAATTCAGAT 808
794 TTACTGAT 833
809 CTATTCAT 868
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869 CAAGAGAGAGAGTGGGCTGAGAGAGTGGGCTGAGAGAGTGGGCTGAGAGAGTGGGCTGAG 928
914 GATCAGATGAGATCT 973
929 GATCAGATGAGATCT 988
974 CATTTGACAGATGAGATCT 1033
989 CACTGTGACAGATGAGATCT 1048
1034 CCCCATCTCTATGAGTCT 1093
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1094 CTCATGAGAGAGAGTGGGCTGAGAGAGTGGGCTGAGAGAGTGGGCTGAGAGAGTGGGCTG 1153

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1154 TTCCGTCCTCAGAGAGAGTGGGCTGAGAGAGTGGGCTGAGAGAGTGGGCTGAGAGAGTGG 1213
1169 ATCTGTTTCCAGAGAGTGGGCTGAGAGAGTGGGCTGAGAGAGTGGGCTGAGAGAGTGG 1226
1214 CTAT 1273
1227 -----AGACTTTTAT 1279
1274 ATAGAGAGTGGGCTGAGAGAGTGGGCTGAGAGAGTGGGCTGAGAGAGTGGGCTGAGAG 1298
1280 ATAAAGAGTGGGCTGAGAGAGTGGGCTGAGAGAGTGGGCTGAGAGAGTGGGCTGAGAG 1304

RESULT 15
US-09-088-337B-45
Sequence 45, Application US/09088337B
Patent No. 6348574
GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
Gray, Patrick W.
Schweikart, Vicki L.
TITLE OF INVENTION: No. 6348574el Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
City: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/088,337B
FILING DATE: 01-Jun-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/153,848
FILING DATE: 17-Nov-1993
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-Nov-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 6348574and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31794
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 1317 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 201..1211
SEQUENCE DESCRIPTION: SEQ ID NO: 45:
US-09-088-337B-45
Query Match 44.5%; Score 834.6; DB 4; Length 1317;
Best Local Similarity 83.9%; Pred. No. 2.6e-159;
Matches 977; Conservative 0; Mismatches 164; Indels 24; Gaps 2;

[illegible]

Db	1227	-----AGACTTTT	TATACGATAA	TAACTTTT	TATAGTTAC	ATTTTCAGAT	1279
QY	1274	ATAAGAGACT	GACCAGCTT	GTGTACA	1298		
Db	1280	ATTAAGAGCT	GACCAATTT	GAANA	1304		

Search completed: July 12, 2003, 16:00:12
Job time : 90 secs

GenCore version 5.1.6
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OM protein - nucleic search/ using frame_plus_p2n model

Run on: July 12, 2003, 16:00:18 ; Search time 2185 seconds

(without alignments)
4781.651 Million cell updates/sec

Title: US-09-367-052-2

Perfect score: 1867

Sequence: 1 MEPIVSIVSYSDNYSSEVGS.....KRGSHSVSTSESSSFHSS 359

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5

Ygapop 10.0 , Ygapext 0.5

Delop 6.0 , Delext 7.0

Searched: 2054640 segs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-O=/cgn2_1/USPTO.spool/US09367052/runat_10072003-100044-10351/app-query.fasta_1.519
-DB=GenDbml -OFMT=fastap -SOFIX=rgc -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blsum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR.SCORE=pct -THR.MAX=100 -THR.MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pic -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09367052 -CGN_1_1-1687 -ernat_10072003-100044-10351 -NCPU=6 -ICPU=3
-NO_MMAR -LARGEMEMORY -NEG.SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV.TIMEOUT=120 -WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenBml:*
1: gb_ba:*
2: gb_hcg:*
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6: gb_pat:*
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8: gb_pl:*
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14: gb_vi:*
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16: em_fun:*
17: em_hum:*
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29: em_vi:*
30: em_htg_hum:*
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35: em_htg_rnd:*
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41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1867	100.0	1223	10	MMU59760
2	1867	100.0	1817	10	BC031665
3	1867	100.0	1877	10	D87747
4	1866	99.9	1575	10	MMLESTRPT
5	1866	99.9	1809	10	AB000803
6	1848	99.0	1180	10	MMLCRI2
7	1836	98.3	1422	10	MMLCRI3
8	1836	98.3	3366	10	MMU65580
9	1835	98.3	3770	10	MMLESTRCN
10	1758.5	94.2	1050	10	AF452185
11	1744.5	93.4	1050	10	RNU90610
12	1686.5	90.3	1059	9	AF031089
13	1683.5	90.2	1087	9	AF001928
14	1679.5	90.0	1068	9	AB015943
15	1679.5	90.0	1078	9	DB6579
16	1678.5	89.9	1044	9	AF172234
17	1678.5	89.9	1059	6	AX256185
18	1678.5	89.9	1059	6	AX482330
19	1678.5	89.9	1059	9	AF025375
20	1678.5	89.9	1087	9	PTU89798
21	1678.5	89.9	1225	9	HUMNYRECA
22	1678.5	89.9	1637	9	HUMSTR
23	1678.5	89.9	1645	9	HSNPTFLA
24	1678.5	89.9	1664	6	E37853
25	1678.5	89.9	1664	9	HUMHMB9
26	1678.5	89.9	1664	11	G28514
27	1678.5	89.9	1670	6	AX409496
28	1678.5	89.9	1670	9	HUMGPCR
29	1678.5	89.9	1679	6	AX287116
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31	1678.5	89.9	1737	6	AR015970
32	1678.5	89.9	1737	6	AR060748
33	1678.5	89.9	1737	6	AR070433
34	1678.5	89.9	1737	6	AR103430
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36	1678.5	89.9	1737	6	124455
37	1677.5	89.9	1044	9	AF172216
38	1677.5	89.8	1044	9	AF172210
39	1676.5	89.8	1044	9	AF172211
40	1676.5	89.8	1044	9	AF172212
41	1676.5	89.8	1044	9	AF172213
42	1676.5	89.8	1044	9	AF172214
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RESULT 1

ALIGNMENTS

MMU59760 1223 bp mRNA linear ROD 09-SEP-1996
LOCUS MMU59760
DEFINITION Mus musculus fusin homolog mRNA, complete cds.
ACCESSION U59760
VERSION U59760.1 GI:1527134
KEYWORDS
SOURCE Mus musculus.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 1223)
Heesen, M., Berman, M.A., Gerard, C. and Dorf, M.E.
Cloning of the mouse homologue of the human HIV co-factor gene,
fusin
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1223)
AUTHORS Heesen, M., Berman, M.A., Gerard, C. and Dorf, M.E.
TITLE Direct Submission
JOURNAL Submitted (02-JUN-1996) Pathology, Harvard Medical School, 200
Longwood Avenue, Boston, MA 02115, USA
LOCATION/Qualifiers
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BASE COUNT 285 a 342 c 268 g 328 t
ORIGIN
Alignment Scores:
Pred. No.: 2.73e-178 Length: 1223
Score: 1867.00 Matches: 359
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Indels: 0
Gaps: 0
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Qy 141 ValHisAlaThrAsnSerGlnArgProArgLysLeuLeuAlaGluLysAlaValTyrVal 160
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Qy 161 GlyValTyrPheProAlaLeuLeuThrIleProAspPheIlePheAlaAspValSer 180
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Db 630 CTGTGATGTGTGTGTTCAATTCACATATATGTTGGGTCTCATCTCCCGGATC 689
Qy 221 ValIleLeuSerCysTyrCysIleIleIleSerLysLeuSerHisSerLysGlyHisGln 240
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Qy 241 LysArgLysAlaLeuLysThrThrValIleLeuIleLeuAlaPhePheAlaCysTyrPhe 260
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Qy 261 ProTyrTyrValGlyIleSerIleAspSerPheIleLeuLeuGlyValIleLysGlnGly 280
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Db 870 TGTACTTCGAGACATCTGACACAGATGATCTCTCATCAACAGAGCCCTGCTCTTC 929
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RESULT 2
BC031665 1817 bp mRNA linear ROD 07-AUG-2002
LOCUS BC031665
DEFINITION Mus musculus, chemokine (C-X-C) receptor 4, clone MGC:36266
IMAGE:3592479, mRNA, complete cds.
ACCESSION BC031665
VERSION BC031665.1 GI:21618781
KEYWORDS MGC.
SOURCE house mouse.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1817)
Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (06-JUN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgabs-remail.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
 DNA Sequencing by: Baylor College of Medicine Human Genome
 Sequencing Center
 Center code: BCM-HGSC
 Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
 Contact: amgdbcm.tmc.edu
 Gunaratne, P.H., Garcia, A.M., Lu, X., Huylk, S.W., Hale, S.M.,
 Yoon, V.S., Kovis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.,
 Richards, S., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LIML at: <http://image.liml.gov>
 Series: IRAX Plate: 61 Row: d Column: 24
 This clone was selected for full length sequencing because it
 passed the following selection criteria: Similarity but not
 identity to protein.

FEATURES

Location/Qualifiers
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 /db_xref="LocusID:12767"
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CDS

BASE COUNT 443 a 435 c 396 g 543 t
 ORIGIN

Alignment Scores:

Prod. No.: 4.23e-178 Length: 1817
 Ident. Similarity: 1867.00 Matches: 359
 Local Similarity: 100.00% Conservative: 0
 Query Match: 100.00% Mismatches: 0
 DB: 10 Indels: 0 Gaps: 0

US-09-367-052-2 (1-359) x BC031665 (1-1817)

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 DB 78 ATGAGACCGATCAGTGTATATACACTTCTGTACTCTCTGAGAGAGAGTGGGCT 137
 OY 21 GlyAspTyrAspSerAsnLysGluProCysPheArgAspGluAsnValHisPheAsnArg 40
 DB 138 GGAGACTATGATCCCAACAGGAACCCCTGCTCCGGATGAAGAACGTCATTTCATAGG 197
 OY 41 IlePheLeuProThrIleTyrPheIleIlePheLeuThrGlyIleValGlyAsnGlyLeu 60
 DB 198 ATCTTCCCTGCCACCATCTACTCTCATCTCTTCTGATGCGCATAGTCGGCAATGGATTG 257
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 DB 258 GTGATCCTGGTCAATGGTTACCAAGAGAGCTAAGGACATGACGACAGATACGGCTG 317
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DB 318 CACCTGACAGTGGCTGACCTCTCTTGTGATCAACACTCCCTTCTGGGAGTTGATGCC 377
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 DB 438 AACCTCTACAGCAGCTTCTATCTGCTGCTTCACTACACCTGGACCGGTACTCGCCATT 497
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 OY 321 GlnHisAlaLeuAsnSerMetSerArgLysSerSerLeuLysIleLeuSerLysGlyLys 340
 DB 1038 CAGCATGCACTCAACTCATGAGCAGAGGCTCCACCTCCAGATCCCTTCCAAAGAGAAAG 1097
 OY 341 ArgGlyGlyHisSerSerValSerThrLysSerGluSerSerPheHisSerSer 359
 DB 1098 CGGGGTGACACTCTCTCTCTCCAGGAGTCAAGATCTCCAGTTTCACTCCAGC 1154

RESULT 3
 DB87747
 LOCUS D87747 1877 bp mRNA linear ROD 07-FEB-1999
 DEFINITION Mus musculus mRNA for murine CXCR-4, complete cds.
 ACCESSION D87747.1 GI:1772445
 VERSION D87747.1
 KEYWORDS murine CXCR-4.
 SOURCE Mus musculus bone marrow pre-B cell cell_line:DW34 cDNA to mRNA.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus; Mus.
 1 (sites)
 Nagasawa, T., Nakajima, T., Tachibana, K., Itasaka, H., Bleul, C.C.,
 Yoshie, O., Matsushima, K., Yoshida, N., Springer, T.A. and
 Kishimoto, A.
 Molecular cloning and characterization of a murine pre-B-cell
 growth-stimulating factor/stromal cell-derived factor 1 receptor, a
 murine homolog of the human immunodeficiency virus 1 entry
 coreceptor fusin

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 93 (25), 14726-14729 (1996)
 MEDLINE 97121456
 REFERENCE 2 (bases 1 to 1877)
 AUTHORS Nagasawa, T. T.
 TITLE Molecular cloning of murine PBSF/SDF-1 receptor
 JOURNAL Unpublished
 REFERENCE 3 (bases 1 to 1877)
 AUTHORS Nagasawa, T.
 TITLE Direct Submission
 JOURNAL Submitted (05-SEP-1996) Takashi Nagasawa, Research Institute, Osaka
 Medical Center, Department of Immunology, Murdoccho 840, Izumi,
 Osaka 590-02, Japan (E-mail: immunol@osk.ri.medic.ac.jp,
 Tel: 0725-56-1220, Fax: 0725-57-3021)
 Location/Qualifiers

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BASE COUNT 469 a 450 c 407 g 551 t
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Alignment Scores:

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 Best Local Similarity: 100.00% Mismatches: 0
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 DEFINITION receptor.
 ACCESSION X99582.1 GI:1666648
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 KEYWORDS leu gene; leukocyte-derived seven transmembrane domain receptor.
 SOURCE Mus musculus.
 ORGANISM Mus musculus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 1575)
 REFERENCES
 1 Moepfs, B., Frodl, R., Kessler, H. and Gierschik, P.
 cDNA cloning and genomic organization of a leukocyte-derived seven
 transmembrane domain receptor (LEST) from mouse: a murine
 homologue of the human HIV-1 entry cofactor fusin
 Unpublished
 2 (bases 1 to 1575)
 REFERENCES
 1 Moepfs, B.
 Direct Submission
 JOURNAL Submitted (19-JUL-1996) B. Moepfs, Universitaet Ulm,
 Pharmacology/Toxicology, Albert-Einstein Allee 11, D-89081 Ulm, FRG
 TITLE JOURNAL
 REMARK Revised by author 11-NOV-96

COMMENT On Nov 12, 1996 this sequence version replaced gi:1657351.
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 LOCUS Mouse mRNA for murine CXCR-4, complete cds.
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 VERSION AB000803.1
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 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 1809)
 AUTHORS Suzuki, G., Nakata, Y., Uzuwa, A., Shitasawa, T., Saito, T. and Mita, K.
 TITLE Molecular cloning of murine CXCR-4, a murine homologue of HIV entry
 co-receptor, that is expressed on leukocyte and other organs
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 1809)
 AUTHORS Suzuki, G.
 TITLE Direct Submission
 JOURNAL Submitted (29-JAN-1997) Gen Suzuki, National Institute of
 Radiological Sciences, Division of Radiation Health; 4-9-1,
 Anagawa, Inage-ku, Chiba, Chiba 263, Japan
 (E-mail:gsuzuki@umx1.nirs.go.jp, Tel:043-251-2111,
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Alignment Scores:

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US-09-367-052-2 (1-359) x AB000803 (1-1809)

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DB 252 GTGATCCGTGGTCATGCGTTACAGAGAAAGCTAAGACATAGCGAGACAGTACGGCTG 311
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VERSION Z80112.1 GI:2632100
KEYWORDS CXC chemokine receptor 4; CXCR-4; lcr-1 gene.
SOURCE Mus musculus.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 1180)
Schubel, A., Burgstahler, R. and Lipp, M.
The mouse homologue of the human HIV coreceptor CXCR-4 (FUSIN):
High expression in thymus and lymphoid tissues
unpublished
2 (bases 1 to 1180)
Lipp, M.
Direct Submission
Submitted (11-SEP-1996) Martin Lipp, Max-Deibnick-Center for
Molecular Medicine, MDC, Robert-Roessle-Strasse 10, BERLIN-BUCH,
D-13122 GERMANY
On Nov 21, 1997 this sequence version replaced gi:1542888.

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JOURNAL
AUTHORS
TITLE
REFERENCE
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US-09-367-052-2 (1-359) x MMLCR12 (1-1180)

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    OY 301 HisCysCysLeuAsnProIleLeuTyrAlaPheLeuGlnAlaLysPheLysSerSerAla 320
    895 CACTGTTCCTGAGAACCCCATCTCTATGCTTCTCTGGGGGCCAAGTCAAAAGCTCTGCC 954
    OY 321 GlnHisAlaLeuAsnSerMetSerArgLysSerSerLeuLysIleLeuSerLysGlyLys 340
    955 CAGCATGCACTCACTCATCATGACAGAGGCTCCAGCTCCTCAAGATCTTTCCAAAGGAAAG 1014
    OY 341 ArgGlyGlnHisSerSerValSerThrGluSerGluSerSerSerPheHisSerSer 359
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RESULT 7
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LOCUS MMLCR13 1422 bp DNA linear ROD 31-OCT-1996
DEFINITION Mus musculus lcr-1 gene, exon 2.
ACCESSION 280113
VERSION 280113.1 GI:1655638
KEYWORDS CXC chemokine receptor 4; CXCR-4; lcr-1 gene.
SOURCE Mus musculus.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1422)
Schubel, A., Burgstahler, R. and Lipp, M.
The mouse homologue of the human HIV coreceptor CXCR-4 (FUSIN): High expression in thymus and lymphoid tissues
Unpublished
JOURNAL 2 (bases 1 to 1422)
REFERENCE
AUTHORS Lipp, M.
TITLE Direct Submission
JOURNAL Submitted (11-SEP-1996) Martin Lipp, Max-Deiblbrueck-Center for Molecular Medicine, MDC, Robert-Roessle-Strasse 10, BERLIN-BUCH, D-13122, GERMANY
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Alignment Scores:
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Score: 1836.00 Matches: 354
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Best Local Similarity: 98.88% Mismatches: 1
Query Match: 98.34% Indels: 1
DB: 10 Gaps: 0

US-09-367-052-2 (1-359) x MMLCR13 (1-1422)

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Db      364 CCTCCACCAACCTTCTCATCTCTTGTACGTGGCATATCGGCATATGATGGATGGCAT 423
Oy      62 eleuValMetGlyIleGlySngIleValArgSerMetThrSpsIleThyrAlaGlyLeuIle 82
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Oy      182 yAspIleSerGlnIleValAspAspArgTyrIleCysAspArgLeuTyrProAspSerLeuTr 202
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KEYWORDS
SOURCE      Mus musculus.
ORGANISM    Mus musculus.
REFERENCE   1 (bases 1 to 3366)
AUTHORS     Heesen,M., Berman,M.A., Benson,J.D., Gerard,C. and Dorf,M.E.
TITLE       Cloning of the mouse fusin gene, homologous to a human HIV-1
            co-factor
JOURNAL     J Immunol. 157 (12), 5455-5460 (1996)
MEDLINE     97113334
PUBMED      8955194
REFERENCE   2 (bases 1 to 3366)
AUTHORS     Heesen,M., Berman,M.A., Gerard,C. and Dorf,M.E.
TITLE       Direct Submission
JOURNAL     Submitted (30-JUL-1996) Pathology, Harvard Medical School, 200
            Longwood Avenue, Boston, MA 02115, USA
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Best Local Similarity: 98.88%      Mismatches:      1
Query Match:    98.34%      Indels:      1
DB:            10      Gaps:      0
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Db      2292 CCTGTTCCCTTTGCAGATATATCACTCTGATAACTACTGCAAGACAGTGGGCTCGAGA 2351
Oy      22 pTyrAspSerAsnLysGluProCysPheArgGspGluAsnValHisPheAsnArgIlePhe 42
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 Db 2472 CCGGGTCATGGGTACAGAGAGAGCTAAGAGAGATGACAGACAGTACCGCGCTGCACCT 2531
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 DEFINITION domain receptor, strain B6.
 ACCESSION X99581
 VERSION X99581.1 GI:1924959
 KEYWORDS lestr gene; leukocyte-derived seven transmembrane domain receptor.

SOURCE Mus musculus.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 3770)
 AUTHORS Moepks,B., Frodl,R., Kessler,H. and Gierschik,P.
 TITLE cDNA cloning and genomic organization of a leukocyte-derived seven transmembrane domain receptor (LESTR) from mouse: a murine homologue of the human HIV-1 entry cofactor fusin
 JOURNAL unpublished
 REFERENCE 2 (bases 1 to 3770)
 AUTHORS Moepks,B.
 TITLE Direct Submission
 JOURNAL Submitted (19-JUL-1996) B. Moepks, Universitaet Ulm,
 Pharmacology/Toxicology, Albert-Einstein Allee 11, D-89081 Ulm, FRG
 REMARK 3 (bases 1 to 3770)
 REFERENCE Moepks,B.
 TITLE Direct Submission
 JOURNAL Submitted (02-APR-1997) B. Moepks, Universitaet Ulm,
 Pharmacology/Toxicology, Albert-Einstein Allee 11, D-89081 Ulm, FRG
 COMMENT On Apr 3, 1997 this sequence version replaced gi:1666646.
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 Percent Similarity: 99.44% Conservative: 3
 Best Local Similarity: 98.60% Mismatches: 1
 Query Match: 98.29% Indels: 1
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 US-09-367-052-2 (1-359) x MMLESTRGN (1-3770)
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LOCUS      AF452185                1050 bp    mRNA    linear    ROD 18-DEC-2001
DEFINITION Rattus norvegicus strain Holtzman chemokine receptor CXCR4 (Cxcr4)
ACCESSION  AF452185
VERSION    AF452185.1  GI:17902280
KEYWORDS
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    Rattus norvegicus.
    Rattus norvegicus.
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
    Rattus.
REFERENCE  1 (bases 1 to 1050)
AUTHORS   Simen,A.A. and Miller,R.J.
TITLE      Chemokine regulation of neuronal signaling and gp120 neurotoxicity
JOURNAL    Unpublished
REFERENCE  2 (bases 1 to 1050)
AUTHORS   Simen,A.A. and Miller,R.J.
TITLE      Direct Submision
JOURNAL    Submitted (25-NOV-2001) Dept. Psychiatry, Yale University, New
            Haven, CT 06508, USA

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Score:          1758.50      Matches:      340
Percent Similarity: 97.18%      Conservative: 4
Best Local Similarity: 96.05%      Mismatches: 5
Query Match:      94.19%      Indels:      5
DB:              10      Gaps:      1

US-09-367-052-2 (1-359) x AF452185 (1-1050)
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QY      46  lIleTyrrPheIleIlePheLeuThrGlyIleValGlyAsnGlyLeuValIleLeuValMet 65
Db      121  ATCTATTTTATCATCTTCTTGACTGGCATAGAGGGGCAAAAGGTTGTGTAATCTCTGGTCATG 180
QY      66  gLTYrGlnLysLysLeuArgSerMetThrAspLysTyrrArgLeuHisLeuSerValAla 85

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Oy      126 ValleunleuleualaphelleSerleuasparglyrleualallevalhisalathrasn 145
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Oy      146 SerGlnarproarglylsleuleualaglulysalavalalyrvalaglyvaltrpIlepro 165
Db      421 AGCCAGAGGCGGAGAGAGCTGCTGGTGAAGAGCGCTCATGTGGGTGTCTGGATCCC 480
Oy      166 AlaleuleuleuthrilleproaspheillephealaspvalserGlnglyAspIleSer 185
Db      481 GCCCTCTCTCGATATCCCGACATCATCTTGGCCGATGTC-----AGC 525
Oy      186 GlnGlyaspasparglyrIleCysaspargleuTytrProaspserleuTytrmetValVal 205
Db      526 CAGGGGAGCGGAGAGCTACATCTGTGACCGGCTTACCAGCAGACCTGTGGATGGTGTG 585
Oy      206 PheGlnpheGlnhisIleMetValGlyleuleuleuproglyIleValIleleuSerCys 225
Db      586 TTCAGTTCACAGCATCATCATGTGGGTGTCTATCTCGGGGACATGTCATCTGCTGT 645
Oy      226 TyrcysIlellelleSerlysleuSerHisSerlysGlnhisGlnlysalarglysalaleu 245
Db      646 TACGTCATCATCATCTCCAGCTGTCTACACTCCAGAGGCCACGAAAGCCGACAGCCCTC 705
Oy      246 LysThrThrValIleleuleuleualaphenhealacystIleuproTytrTytrValGly 265
Db      706 AAGCTACAGGTCACTTATCTGCTGCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTG 765
Oy      266 IleSerIleaspserPheIleleuleuleuGlyValIlelysglnGlyCysaspheGluSer 285
Db      766 ATCGCATCATCTCTCATCTCTTGTGAGGTCTTCACAGCAAGGATGTGATTTGGAAGC 825
Oy      286 IleValHislystrPileSerIleThrGluAlaleualaphenheHisCysCysleuAsn 305
Db      826 GTCTGTGACAAAGTGCATCTCATACGAGAGCCCTCCCTTCTTCCACTGTGCTTAC 885
Oy      306 ProIleleuTyralaphelauGlyAlaLysPheLysSerSerAlaGlnHisAlaLeuAsn 325
Db      886 CCCATCTCTACGCTTCTCTCGGGGCAAAATTCAGAGCTCCGCGCAGCATGCACATCAT 945
Oy      326 SerSerSerArgGlySerSerleuLysIleleuSerlysGlyLysArgGlyGlyHisSer 345
Db      946 TCATGTGACAGAGGCTCCACCTCAAGATCTTTCCAAAGGGAACCGGGGTGACACTCT 1005
Oy      346 SerValSerThrGlnSerGlnSerSerSerPheHisSerSer 359
Db      1006 TCCGTCTCCACAGAGTCAAGATCTCTCAAGTTTTCATCTCCAGC 1047

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RESULT 11
RNU90610      1050 bp mRNA linear ROD 26-MAR-1997
LOCUS         Rattus norvegicus CXc chemokine receptor (CXCR4) mRNA, complete
DEFINITION   cds.
ACCESSION    U90610
VERSION      U90610.1 GI:1906612
KEYWORDS
SOURCE       Rattus norvegicus.
ORGANISM     Rattus norvegicus.
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
              Rattus.
REFERENCE    1 (bases 1 to 1050)

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AUTHORS      Harrison, J.K. and Salafianca, M.N.
TITLE        Molecular cloning of rat CXCR4
JOURNAL      Unpublished
REFERENCE    2 (bases 1 to 1050)
AUTHORS      Harrison, J.K. and Salafianca, M.N.
TITLE        Direct Submission
JOURNAL      Submitted (25-FEB-1997) Pharmacology and Therapeutics, University
              of Florida, 1600 SW Archer Rd., Gainesville, FL 32610-0267, USA
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1..1050
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/product="CXc chemokine receptor"
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KFLCKAVHIIYTNLYSVLILAFISLDRFLVHVATNSQARKLAEKAVYGVNIP
ALLITPDILFADVDSQGRVITCDRLYPPDSIAMVVFQFQIMVGLIPGVITISCT
IISKLSKSKHOKRKALKTYVILILAFACWLEPYVYGISIDSTILEVIRKGFESV
VHWKSTLEALFAFHCCNPLILYAFGLAKFKSSAONALNSMSSSLIKSKRGKH
SVSTSESSSFSS"
BASE COUNT   231 a      313 c      247 g      259 t
ORIGIN
Alignment Scores:
Pred. No.:    4.77e-166      Length:    1050
Score:        1744.50       Matches:    338
Percent Similarity: 96.61%   Conservative: 4
Best local Similarity: 95.48% Mismatches: 7
Query Match:  93.44%      Indels:    5
DB:            10          Gaps:    1
US-09-367-052-2 (1-359) x RNU90610 (1-1050)
Oy      6 ValSerIleTytrThrSerAsparGlySerGlnGluValGlySerGlyAspTyraSPSer 25
Db      1 ATGGAATATACATCTTGATTAAGTACTCCGAGAAATAGGCTGAGAGCTATGACTCC 60
Oy      26 AsnlyGluProCysPheArgAspGluAsnValHisPheAsnArgIlePheLeuProThr 45
Db      61 AACAGAGAACCTGCTCCGGAGTGAAGAAAGAAACTTCAGAGAGATCTTCCGCCACC 120
Oy      46 IleTyThrIlellePheleuThrGlyIleValGlyAsnGlyleuValIleleuValmet 65
Db      121 ATCTATTTTATCATCTTCTTGACGCGCATGTGGGCAANTGGGTGGTGAATCTCGTCATG 180
Oy      66 GLTTCGlnlyslsleuArgSerMetThrAspLysTytrArgLeuHisleuSerValAla 85
Db      181 GGTACCAGAGAAGAGCTGAGAGCATACAGACAGTACCGGCTGACCTGTCCGTGGCT 240
Oy      86 Aspleuleuphevaliethrleuprophetralavalasplametalasptprtyr 105
Db      241 GACCTCTCTTTGTCATCACACATCCCTCTGGGACATGAGCGCATGGCTGACTGGTAC 300
Oy      106 PheglylyspheleucyslysalavalahisilellythrvalasleuTySerSer 125
Db      301 TTTGGGAATTTTATATAGAGCTGTGCATATATCATCTACACCGCATCTTACAGCAGT 360
Oy      126 ValleunleuleualaphelleSerleuasparglyrleualallevalhisalathrasn 145
Db      361 GTTCTCATCTCTGGCTTCATCAGCTGACCGGCTTACCTGCATTTGCCAGCCACCAAC 420
Oy      146 SerGlnarproarglylsleuleualaglulysalavalalyrvalaglyvaltrpIlepro 165

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Db      421 AGCCAGAGCGGAGAGCTGCTGCTGAAAAGCCGCTATGTGGTGTGATGCC 480
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Db      481 GCCCTCTCTCCGACTATCCCGACATCATCTTCCCATGTC-----AGC 525
Qy      186 GlnGlyaspAspArgTyrIleCysaspArgLeuTyrProaspSerLeuTyrPheValVal 205
Db      526 CAGGGGAGGAGGAGAGTACATCTGTGACCGGCTTACCAGCCAGACAGCTGTGATGTGTG 585
Qy      206 PheGlnPheGlnHisIleMetValGlyLeuIleLeuProGlyIleValIleLeuSerCys 225
Db      586 TTCACAGTTCACGACATCATCTGTGCTCATCTCTGCGGCGCATCGTATCTGCTCTGT 645
Qy      226 TyrCysIleIleIleSerLysSerLysSerHisSerLysGlyHisGlnLysArgLysAlaLeu 245
Db      646 TACGTCATCATCTCTCCAGCTTCACACTCCAGAGGCCACCAAGAGCCAGAGGCCCTTC 705
Qy      246 LysThrThrValIleLeuIleLeuAlaPhePheAlaCysThrPheLeuProTyrTyrValGly 265
Db      706 AAGACTAGCGTCACTTATCTCTGCTGCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTG 765
Qy      306 ProIleLeuTyrAlaPheLeuGlyAlaLysPheLysSerSerAlaGlnHisAlaLeuAsn 325
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Qy      326 SerIleSerArgGlySerSerLeuLysIleLeuSerLysGlyLysArgGlyHisSer 345
Db      946 TCCATGAGCAGAGGCTCAGGCTCAAGATCTTTCACAAAGGAGGAGGAGGAGGAGGAG 1005
Qy      346 SerValSerThrGlnSerGlnSerSerSerPheHisSerSer 359
Db      1006 TCCGCTCTCCACAGAGTCAAGATCTTCAAGTTTTCACCTCCAGC 1047

RESULT 12
AF031089      1059 bp      mRNA      linear      PRI 14-OCT-1998
DEFINITION   Papio hamadryas anubis CXc chemokine receptor 4 (CXCR4) mRNA,
ACCESSION    AF031089
VERSION      AF031089.1 GI:2625093
SOURCE       Papio cynocephalus anubis.
ORGANISM     Papio cynocephalus anubis.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
Cercopithecinae; Papio.
REFERENCE    1 (bases 1 to 1059)
AUTHORS      Benton, P.A., Lee, D.R. and Kennedy, R.C.
TITLE        Sequence comparisons of non-human primate HIV-1 coreceptor
JOURNAL      Mol. Immunol. 35 (2), 95-101 (1998)
MEDLINE      98346785
PUBMED       9683255
REFERENCE    2 (bases 1 to 1059)
AUTHORS      Benton, P.A. and Kennedy, R.C.
TITLE        Direct Submission
JOURNAL      Submitted (22-OCT-1997) Microbiology and Immunology, University of
Oklahoma Health Sciences Center, 800 Research Parkway, Rm 458,
Oklahoma City, OK 73104, USA
FEATURES     location/Qualifiers
SOURCE       1..1059
              /organism="Papio cynocephalus anubis"
              /sub_species="anubis"
              /db_xref="taxon:9535"

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QY 246 LysThrThrValIleLeuIleLeuAlaIlePhePheAlaCysTrpLeuProTyrTyrValGly 265
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Db 715 AAGACCGAGGTCATCCATCCATCCGCTTCTCCGCTGCGCGCTTATATACATTGGG 774
QY 266 IleSerIleAspSerPheIleLeuLeuGlyValIleLysGlnGlyCysAspPheGluSer 285
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Db 775 ATCAGTATCCAGCTCTTCATCTCTCTGGAATCATCATCAAGAGGCTGATTTGAGAAC 834
QY 286 IleValHisLysTrpIleSerIleThrGlnAlaLeuAlaPhePheHisCysCysLeuAsn 305
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QY 306 ProIleLeuTyrAlaPheLeuGlyAlaLysPheLysSerAlaGlnHisAlaLeuAsn 325
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Db 895 CCCATCCCTATGCTTCTTCTGGAGCCAAATTTAAACCTCTGCCACGACGACTCCACC 954
QY 326 SerMetSerArgLysSerSerLeuLysIleLeuSerLysGlyLysArgGlyLysIleSer 345
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Db 955 TCTGTGACGACAGGCTCCAGCTCAAGATCTCTCTCCAAAGAAAGCGAGGGGACATTCCG 1014
QY 346 SerValSerThrGlnSerGlnSerSerSerPheHisSerSer 359
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Db 1015 TCTGTTCCACTGAGTCTGAGTCTTCAAGTTTTCACCTCCACC 1056
RESULT 13
AF001928 1087 bp mRNA linear PRI 10-MAR-1998
LOCUS Macaca mulatta alpha-chemokine receptor 4 (CXCR4) mRNA, complete cds.
DEFINITION
ACCESSION AF001928
VERSION AF001928.1 GI:2911293
KEYWORDS
SOURCE Macaca mulatta.
ORGANISM Macaca mulatta.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
Cercopithecinae; Macaca.
REFERENCE
AUTHORS Pretel,J.L., Guillot,J.G. and Butor,C.
TITLE New widespread CXCR4 allele in rhesus macaques does not predict
subspecies or clinical evolution
JOURNAL AIDS Res. Hum. Retroviruses 14 (7), 639-641 (1998)
MEDLINE 98252393
PUBMED 9591719
2 (bases 1 to 1087)
DIRECT PRETEL,J.-L., Guillot,J.-G. and Butor,C.
TITLE Direct Submission
JOURNAL Submitted (01-MAY-1997) INSERM U445, ICGM, 22 rue Mechain, Paris
75014, France
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Alignment Scores:
Pred. No.: 6,72e-160 Length: 1087
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Best Local Similarity: 90.40% Mismatches: 12
Query Match: 90.17% Indels: 5
Gaps: 1
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QY 86 AspleuLeuPheValIleThrLeuProPheThrPalValAlaMetAlaAspTyrPyr 105
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QY 166 AlaLeuLeuLeuThrIleProAspPheIlePheAlaAspValSerGlnGlyAspIleSer 185
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Db 518 GCCCTCCGCTGACATATCCCGACTCATCTTTGGCACCGTC -----AGT 562
QY 186 GlnGlyAspAspArgTyrIleCysAspArgLeuTyrProAspSerLeuTrpMetValAla 205
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Db 563 GAGCGAGATGACAGTATATCTGTACCGCTTCTTACCCCAATGACTTGTGGGTGGTTCG 622
QY 206 PheGlnPheGlnHisIleMetValGlyLeuIleLeuProGlyIleValIleLeuSerCys 225
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Db 623 TTCCAGTTTACGACATCATGATGTTGGCTTATCCGCTGGATGTCATCCTGTGCTGC 682
QY 226 TyrcysllellelleSerLysLeuSerHisSerLysGlnGlnLysArgLysAlaLeu 245
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Db 683 TATTGCATTTATCATCTCCAGCTGCACACTCCCAAGGGCCACGAAACGCGACGCCCTC 742
QY 246 LysThrThrValIleLeuIleLeuAlaPhePheAlaCysTrpLeuProTyrTyrValGly 265
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Db 743 AAGACCGAGGTCATCTCATCTGCTTCTTCTGCTGCTGCTGCTTATATACATTGGG 802
QY 266 IleSerIleAspSerPheIleLeuLeuGlyValIleLysGlnGlyCysAspPheGluSer 285
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QY 286 IleValHisLysTrpIleSerIleThrGlnAlaLeuAlaPhePheHisCysCysLeuAsn 305
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Db 923 CCCATCTCTATGCTTCTTCTTGAGCAATTTAAACCTCTGCGGACGACTAC 982
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Db 1043 TCTGTTCACAGTGAGTGTGAGTCTTCAAGTTTTCACACGAC 1084

RESULT 14
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LOCUS Chlorocebus aethiops mRNA for CXCR4 receptor, complete cds.
DEFINITION AB015943 GI:3294341
ACCESSION AB015943.1
VERSION 1
KEYWORDS CXCR4 receptor.
SOURCE Chlorocebus aethiops cDNA to mRNA.
ORGANISM Ceropithecus aethiops
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Ceropithecidae;
Ceropithecinae; Ceropithecus.
REFERENCE 1 (bases 1 to 1068)
Murrayama, Y., Matsunaga, S. and Inoue-Murayama, M.
cDNA sequence of African green monkey CXCR-4 chemokine receptor
gene
JOURNAL Published Only in Database (1998)
REFERENCE 2 (bases 1 to 1068)
Murrayama, Y., Matsunaga, S. and Inoue-Murayama, M.
Direct Submission
TITLE Submitted (01-JUL-1998) Yuichi Murrayama, National Institute of
Animal Health, Food Safety Research Laboratory, Kannondai 3-1-1,
Tsukuba, Ibaraki 305-0856, Japan (E-mail: mtspoke@nrc.mhn.or.jp,
Tel:+81-298-38-7840, Fax:+81-298-38-7825)
location/Qualifiers
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BASE COUNT 241 a 300 c 237 g 290 t
ORIGIN
Alignment Scores:
Pred. No.: 1.66e-159 Length: 1068
Score: 1679.50 Matches: 320
Percent Similarity: 94.92% Conservative: 16
Best Local Similarity: 90.40% Mismatches: 13
Query Match: 89.96% Indels: 5
Gaps: 1

US-09-367-052-2 (1-359) x AB015943 (1-1068)

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Db 70 ATAAAGAACCCCTGCTCCCTGAAGAAAATGCTCATTTCAATAGATCTTCCGCCAC 129
Qy 46 IletyRPhelIethleuethrlylevalglyasnlyeuvalleleuvalmet 65
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Qy 66 GLYTYGGLNYSYSLEUAARGSERMETHRASPLYTYARGLEUHSLEUSERVALA 85
Db 190 GGTACCAGAGAAACTGAGAACATGACGAGACAGACAGCTGACCTGTAGTGGCT 249
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Qy 106 PheglylysPheleucyslysalavalhisIleIetyrThryValasnleutySer 125
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Qy 146 SerGlnarProarglyserleuenualaglulysalavaltyrvalglyaltrpIlepro 165
Db 430 AGTCAAGAGCCAGAGAGAGCTGTGGCTGAAGAGGTGTATGTGTGTGTGTGTGTGTGT 489
Qy 166 AlaleuenuethrIleproasphelIephalaaspvalserglnglyaspIleser 185
Db 490 GCCCTCTGCTGACTATCCCACTTCACTTTTGGCCAGCTC-----AGT 534
Qy 186 GlnGlyAspasparglyrIleCysaspargLeutyProaspserleutrpmetValal 205
Db 535 GAGGCCGATACAGATATATCTGTGACCGCTTACCCCAATACCTTGTGGGTGTGTG 594
Qy 206 PheGlnPheGlnHisIleuetyalGlyleuIleuProGlyIleValIleuSerCys 225
Db 595 TTCCAAATTCAGACATCATCATGCTTGGCTTATCTGCTGATGTGTGTGTGTGTGTGT 654
Qy 226 TyrCysIleIethleuSerleuSerHisserIleuGlyHisGlnlysnarglysalaleu 245
Db 655 TATTTGATTTATCATCTTCCAGCTGTCCACACTCCAAAGGCCACCAAGGCCAGGCCCTC 714
Qy 246 LysThrThryalIleuIleuIleuvalaphelalCysTrpLeuProtyrtyrvalGly 265
Db 715 AAGACCAAGCTCATCTCATCTGCTTCTTGTGCTGCTGCTGCTTATTTATTCATTGG 774
Qy 266 IleSerIleaspserPheIethleuenuGlyvalIleuGlnGlyCysasphegluser 285
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Qy 326 SermetserarglyserSerleuylaleuserylsglylsarglylhisSer 345
Db 955 TCTGTGACAGAGGCTCCAGCTCAGATCTCTCCAAAGAAAGGAGGAGGACTCG 1014
Qy 346 SerValserThrglusergluserSerSerPhehisSer 359
Db 1015 TCTGTTCACAGTGAGTGTGAGTCTTCAAGTTTTCACACGAC 1056

RESULT 15
D86579 1078 bp mRNA linear PRI 07-FEB-1999
LOCUS Macaca fascicularis mRNA for fusin (LESTR), complete cds.
DEFINITION D86579
ACCESSION D86579.1 GI:1468948
VERSION

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: July 12, 2003, 15:58:43 ; Search time 207 Seconds
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Listing first 45 summaries

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-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blomsum2 -TRANS=human40.cdi
-LIST=45 -DOCCALIGN=200 -THR SCORE=PCT -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAYLEN=2000000000
-USER=US09367052_GCGN_1.1_200_etunat_10072003_100043_10328 -NCP=6 -ICP=3
-NO_MMAP -LARGESORTERY -NEG_SCORES=0 -MAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_101002:*

1: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*
2: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
3: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*
4: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
5: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*
6: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:*
7: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:*
8: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:*
9: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:*
10: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:*
11: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:*
12: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:*
13: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:*
14: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:*
15: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:*
16: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:*
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18: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:*
19: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:*
20: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*
21: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query length	DB ID	Description
1	1867	100.0	1758	20	AA227611
2	1867	100.0	1877	19	AAV46370
3	1678.5	89.9	1059	21	AA238553
4	1678.5	89.9	1059	24	AAH99552
5	1678.5	89.9	1588	24	AA227610
6	1678.5	89.9	1664	21	AAA61656
7	1678.5	89.9	1664	21	AA240014
8	1678.5	89.9	1670	24	ABK83803
9	1678.5	89.9	1670	24	ABN5645
10	1678.5	89.9	1679	22	AA165457
11	1678.5	89.9	1679	22	AA080521
12	1678.5	89.9	1737	16	AA080521
13	1678.5	89.9	1737	16	AA099007
14	1672.5	89.6	1059	23	AB197982
15	1672.5	89.6	1317	19	AAV18357
16	1672.5	89.6	1317	21	AAV1726
17	1672.5	89.6	1317	24	ABK54255
18	1672.5	89.6	1944	20	AA155882
19	1672.5	89.6	5161	21	AA20896
20	1672.5	89.6	5161	21	AAA34774
21	1672.5	89.6	5161	21	AAH99551
22	1667.5	89.3	1737	13	AA029506
23	1662.5	89.0	1317	15	AA066179
24	1658.5	88.8	1119	24	AAK98241
25	815	43.7	606	24	ABK92962
26	584	31.3	1107	21	AAA30593
27	584	31.3	1159	20	AA232713
28	584	31.3	1670	19	AAV65557
29	584	31.3	1670	24	ABN97338
30	581.5	31.1	1620	19	AAV3793
31	580	31.1	1107	21	AAA30714
32	575	30.8	1876	18	AAH72800
33	575	30.8	1877	22	AAH55033
34	570.5	30.6	1327	22	ABA09210
35	570.5	30.6	1677	21	AAA58872
36	567.5	30.4	1607	17	AA135277
37	555	29.7	1068	24	ABK16598
38	552	29.6	1068	24	ABK16599
39	551.5	29.5	1200	13	AA030011
40	551.5	29.5	1200	16	AA099949
41	550.5	29.5	1106	16	AA099952
42	550.5	29.5	2072	24	AA517156
43	550.5	29.5	2084	24	ABK54274
44	550.5	29.5	2085	21	AA01745
45	549.5	29.4	1068	24	ABK16592

ALIGNMENTS

RESULT 1
ID AA227611 standard; DNA: 1758 BP.

AC AA227611;

DE Mouse CXCR4 coding sequence.

KW CXCR4; mouse; neovascularisation; inhibitor; solid cancer; therapy;
tissue repairing agent; vascularisation; ss.

OS Mus sp.

XX WO9948528-A1.

XX 30-SEP-1999.

XX 23-MAR-1999: 99WO-JP01448.
 PF
 XX 24-MAR-1998: 98JP-0095448.
 PR
 XX (CHUS) CHUGAI SEIYAKU KK.
 PA (KISH/) KISHIMOTO T.
 XX
 XX Kishimoto T, Nagasawa T, Tachibana K;
 PI
 DR WPI: 1999-591042/50.
 DR P-PSDB: AAY39994.
 XX
 PT Vascularisation Inhibitors -
 PS
 XX Disclosure: Page 50-51: 63pp: Japanese.

This sequence encodes the mouse CXCR4 protein. The invention relates to remedies inhibiting neovascularisation, remedies for solid cancer, remedies for diseases pathologically caused by neovascularisation and tissue repairing agents containing as the active ingredient a substance capable of potentiating CXCR4. Based on a finding that vascularisation is inhibited in a CXCR4 knockout mouse, it becomes possible to prepare remedies inhibiting vascularisation which contain as the active ingredient a substance capable of potentiating CXCR4, remedies for solid cancer, remedies for diseases pathologically caused by neovascularisation and tissue repairing agents containing as the active ingredient a substance capable of potentiating CXCR4. It is also possible to establish methods for treatment with the use of these remedies.

SO Sequence 1758 BP; 447 A; 414 C; 369 G; 528 T; 0 other;

Alignment Scores:
 Pred. No.: 2,54e-209 Length: 1758
 Score: 1867.00 Matches: 359
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 Gaps: 0

US-09-367-052-2 (1-359) x AA27611 (1-1758)

OY 1 MetGluProIleSerValSerIleTyrThrSerAspAsnTyrSerGluGluValGlySer 20
 Db 1 ATGGACCGATCACTGATGATATACACTTCTCATACTGTAAGAGTGGGCTCT 60
 OY 21 GLVAspTyrAspSerAsnLysGluProCysPheArgAspGluAsnValHisPheAsnArg 40
 Db 61 GGAGACTATGACTCCACAAAGAAACCTGCTCCGGGATGAAACGTCCTTAATAGG 120
 OY 41 IlePheLeuProThrIleTyrPheIleIlePheLeuThrGlyIleValGlyAsnGlyLeu 60
 Db 121 ATCTTCTGCGCACACATCTACTTCTATCATCTTCTGACTGGCATAGTCGGCAATGAGTTG 180
 OY 61 ValIleLeuValMetGlyTyrGlnLysLysLeuArgSerMetThrAspLysTyrArgLeu 80
 Db 181 GTGATCTCTGGTCACTGAGGTACCAAGAACGTAAGAGCATGACGACGCGCTG 240
 OY 81 HisLeuSerValAlaAspLeuLeuPheValIleThrLeuProPheTrpAlaValAspAla 100
 Db 241 CACCTGTCACTGGCTGACCTCTTGTATATCACACTCCCTCTTGCGCATGGATGCC 300
 OY 101 MetAlaAspTrpTyrPheGlyLysPheLeuCysLysAlaValHisIleIleTyrThrVal 120
 Db 301 ATGGCTGACTGATCTTGGGAATTTTGTGTAGAGCTGTCCATATCATCTACACGTGC 360
 OY 121 AsnLeuTyrSerSerValLeuIleLeuAlaPheIleSerLeuAspArgTyrLeuAlaIle 140
 Db 361 AACCTTCACAGACGCTTCTCATCTGCTTCATCAGCTGACGCGTACCTCGCCATT 420
 OY 141 ValHisIleThrAsnSerGlnArgProArgLysLeuLeuAlaGluLysAlaValTyrVal 160
 Db 421 GTCCACGCGCACCACTCAAGGCCAAGAAAGCTGCTGCTGAAAGGACAGTCTATGTG 480

OY 161 GlyValTrpIleProAlaLeuLeuThrIleProAspPheIlePheAlaAspValSer 180
 Db 481 GGGCTCTGGATCCAGCCCTCTCTCTACTATACCTTACTTCTTGGCCGATGAC 540
 OY 181 GlnGlyAspIleSerGlnGlyAspAspArgTyrIleCysAspArgLeuTyrProAspSer 200
 Db 541 CAGGCGGACATACATGACGGGGATGACAGGATGACATCTGTGACCGCTTTCACCGATAGC 600
 OY 201 LeuTrpMetValValPheGlnPheGlnHisIleMetValGlyLeuIleLeuProGlyIle 220
 Db 601 CTGTGATGGTGGTTCATTCATTCACATATATGTTGGTGTCTCATCTGCCCGCATC 660
 OY 221 ValIleLeuSerCysTyrCysIleIleIleSerLysLeuSerHisSerLysGlyHisGln 240
 Db 661 GTCATCTCTCTCTTACTGATCATCATCTCTTACGTGTACACACTCCAAAGGCCACAG 720
 OY 241 LysArgLysAlaLeuLysTrpThrValIleLeuIleLeuAlaPhePheAlaCysTrpLeu 260
 Db 721 AAGCGCAAGGCCCTCAGACGACGATCATCTCATCTTCTTGGCTGCTGCTG 780
 OY 261 ProTyrTrpValGlyIleSerIleAspSerPheIleLeuLeuGlyValIleLysGlnGly 280
 Db 781 CCATATTATGTGGGATCAGCATCATGACTCTTCATCTCTTGGAGTCATCAAGCAAGA 840
 OY 281 CysAspPheGluSerIleValHisLysTrpIleSerIleThrGluAlaLeuAlaPhePhe 300
 Db 841 TGTACTCTCAGAGCATCTGTGCACAAATGATCTCCATCACAAGGCCCTCGCTTCTTC 900
 OY 301 HisCysCysLeuAsnProIleLeuTyrAlaPheLeuGlyAlaLysPheLysSerAla 320
 Db 901 CACTGTGTGCTGGAACCCCATCTCTATGCTCTTCTCGGGCCAAAGTTCAAAACCTCGCC 960
 OY 321 GlnHisAlaLeuAsnSerMetSerArgGlySerSerLeuLysIleLeuSerLysGlyLys 340
 Db 961 CAGCATGCACTCAACTCATGATGACGAGGCTCCAGCTCAAGATCTTTCACAAAGGAAG 1020
 OY 341 ArgGlyLysHisSerSerValSerThrGluSerGluSerSerPheHisSerSer 359
 Db 1021 CGGGGTGGACACTTCTCGTCTCCACGAGATCAGAAATCCTCCAGTTTTCATCTCAGC 1077

RESULT 2
 AAV46370 standard; cDNA to mRNA; 1877 BP.
 ID AAV46370
 XX AAV46370:
 AC 20-NOV-1998 (first entry)
 DT XX
 DE Nucleic acid encoding a murine CXC chemokine receptor.
 XX
 KW Mouse; CXC chemokine receptor; pre-B cell line DM34;
 KW CXC chemokine pre-B cell stimulatory factor BSBF/SDP-1;
 KW HIV infection; screening; inhibitor; AIDS; ds.
 XX
 OS Mus sp.
 XX
 FH Key Location/Qualifiers
 FT CDS 120..1199
 FT /*tag= a
 XX
 XX W09835035-A1.
 XX
 PD 13-AUG-1998.
 XX
 PF 07-FEB-1997: 97WO-JP00299.
 XX
 PR 07-FEB-1997: 97WO-JP00299.
 XX
 PA (SHIO) SHIONOGI & CO LTD.
 XX
 PI Iizasa H, Kishimoto T, Nagasawa T, Nakajima T, Tachibana K;
 Yoshida N, Yoshie O;

PT tumors, degenerative disorders, growth deficiencies, hyper- and
PT hypoproliferative disorders, physical trauma, lesions and wounds
XX
PS Disclosure; Fig 14; 138pp: English.

CC This sequence represents cDNA encoding CXCR-4 chemokine receptor-4
CC (CXCR-4). Chemokine receptors play an important role in the chemotaxis of
CC T-cells and phagocytic cells to areas of inflammation. CXCR-4 is a member
CC of the G-protein-coupled receptor family, which is involved in signal
CC transduction, and its ligand is stromal cell derived factor-1 (SDF-1,
CC AAV52508). CXCR-4 also mediates CD4-independent infection by HIV-1.
CC CXCR-4 has now been found to have a role in the aberrant proliferative
CC behaviour of a number of cell types, including numerous primary tumours
CC and derived cell lines. CXCR-4 is involved in cell transformation and
CC tumorigenesis, particularly in brain, breast and colon tumours. It was
CC found to be overexpressed in several brain tumour derived cell lines and
CC primary brain tumour tissues, breast tumour tissues, colorectal
CC adenocarcinoma, lung carcinoma and melanoma cell lines. CXCR-4 expression
CC was required for the continuous proliferation of glioblastoma cancer
CC cells, and inhibition of its gene function resulted in growth arrest.
CC Conversely, overexpression resulted in enhanced and rapid cellular
CC proliferation. CXCR-4 and SDF-1 can be used as markers for the diagnosis
CC and prognosis of cell proliferative disorders, and antisense
CC oligonucleotides complementary to at least a portion of an RNA transcript
CC of a CXCR-4 gene can be used to inhibit hyperproliferation of a tumour
CC cell. Agents that inhibit CXCR-4 function can be used for treating or
CC preventing a disease or disorder involving cell overproliferation, e.g.,
CC brain cancer, breast cancer, colon cancer, prostate cancer and B cell
CC lymphoma, and also premalignant conditions, benign tumours,
CC hyperproliferative disorders, and benign dysproliferative disorders. They
CC can also be used for treating e.g., cirrhosis of the liver, Keldoid
CC formation, psoriasis, benign tumours, fibrocystic conditions and tissue
CC hypertrophy. Compounds that promote CXCR-4 function can also be used for
CC preventing or treating a disease or disorder involving a deficiency in
CC cell proliferation, or treating a condition where cell proliferation
CC would be desirable. Such diseases include degenerative disorders (e.g.,
CC Parkinson's disease, Alzheimer's disease), growth deficiencies,
CC hypoproliferative disorders, physical trauma, lesions (e.g., those caused
CC by ischaemia), and wounds.

XX Sequence 1059 BP; 244 A; 301 C; 232 G; 282 T; 0 other;

Alignment Scores:

Pred. No.: 1,84e-187 Length: 1059
Score: 1678.50 Matches: 319
Percent Similarity: 95.48% Conservative: 19
Best Local Similarity: 90.11% Mismatches: 11
Query Match: 89.90% Indels: 5
Gaps: 1

US-09-367-052-2 (1-359) x AA238553 (1-1059)

OY 6 ValSer11eTyrThrSerAspAsnYrSerGluGluValAlGlySerGlyAspTyrAspSer 25
DB 10 ATCAGATATATACCTTACATACCTACACGAGGAATAGGAGGACATATGATCC 69
OY 26 AsnLysGluProCysPheArGAspGluAsnValHisPheAsnArgIlePheLeuProThr 45
DB 70 ATGACGAGAACCCGTTCCGTGAGAAATCTCAATTCATTAATCTTCGCCGCCACC 129
OY 46 IleTyrPheIleIlePheLeuThrGlyIleValAlGlyAsnGlyLeuValIleLeuValMet 65
DB 130 ATCTACTCATCACTTCCTTAATCTGCAATGTGGCAATGGATGTCATCCGCGCANG 189
OY 66 GLTYrGluLysLysLeuArgSerMetThrAspLysTyrArgLeuHisLeuSerValAla 85
DB 190 GGTTCACAGAAAGAACTTGAGAACATGACGAGACAACTACAGGCTGACCTGACGTGCC 249
OY 86 AspIleLeuPheValIleThrLeuProPheTyrPalaValAspAlaMetAlaAspTyrPyr 105
DB 250 GACCTCCTCTTGTATCATCAGCGTCCCTCTGGCGAGTTGATGCGGTGCAAAAGTGTAC 309
OY 106 PheGlyLysPheLeuCysLysAlaValHisIleIleTyrThrValAsnLeuTyrSerSer 125

DB 310 TTGGGAACTTCTTATGCAAGGACATGATCATCTACAGTCAACCTTACAGCACT 369
OY 126 ValLeuIleLeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThrAsn 145
DB 370 GTTCCTATCTCGCTTTCATCATGTCGACCCCTTACCTGCGCATCTCCACCCACAAAC 429
OY 146 SerGluArgProArgLysLeuLeuAlaGluLysAlaValTyrValGlyValTrpIlePro 165
DB 430 AGTCAGAGGCCAAGAAAGCTGTGGCTGAAGAGTGCTATGTGGCTTGGATCCCT 489
OY 166 AlaLeuLeuLeuThrIleProAspPheIlePheAlaAspValSerGlnGlyAspIleSer 185
DB 490 GCCCTCTCTGCTGATCTTCGACCTCATCTTGCACAGCTC-----ACT 534
OY 186 GlnGlyAspAspArgTyrIleCysAspArgLeuTyrProAspSerLeuTrpMetValVal 205
DB 535 GAGGCAATGACAGATATATCTGTGACCCCTTACCCCAATGACTTGTGGGTGTGTG 594
OY 206 PheGluPheGluHisIleMetValGlyLeuIleLeuProGlyIleValIleLeuSerCys 225
DB 595 TTCCAGTTTCAGCACATCATGTTGGCTTATCTGCTGATTTGTCTATCTCTGCTGTC 654
OY 226 TyrCysIleIleIleSerLysLeuSerHisSerLysGlyHisGlnLysArgLysAlaLeu 245
DB 655 TATTCATTATCATCTCAAGCTGTCACACTCCAAAGGCGCACAGAGCGCAAGGCCCTTC 714
OY 246 LysThrThrValIleLeuLeuLeuAlaPhePheAlaCysTrpLeuProTyrTyrValGly 265
DB 715 AAGACCAACGATATCTTCTGCTTCTTCTGCTGCTGCTGCTTCTTCTTCTTCTTCTTCT 774
OY 266 IleSerIleAspSerPheIleLeuLeuGluGlyValIleGlyGlyCysAspPheGluSer 285
DB 775 ATCAGATGATCTCTTATCTCTCTCGGAATCATCAACAGAGGTGATGAGTTCAGAAC 834
OY 286 IleValHisLysTrpIleSerIleThrGluAlaLeuAlaPhePheHisCysCysLeuAsn 305
DB 835 ACTGTGCACAAAGTGATTCATTCATCCAGGCGCTAGCTTCTTCTCAGCTGTCTGAAC 894
OY 306 ProIleLeuTyrAlaPheLeuGluLysPheLysSerSerAlaGlnHisAlaLeuAsn 325
DB 895 CCCATCTCTATGCTTTCTTCTGAGCCAAATTTAAACCTCTGCGCAGACCCACCTACCC 954
OY 326 SerMetSerArgGlySerSerLeuLysIleLeuSerLysGlyLysArgLysIleHisSer 345
DB 955 TCTGTAGCAGAGGGGTCAGCCTCAAGATCTCTCCAAAGAAAGAGAGGTGACATTTCA 1014
OY 346 SerValSerThrGluSerGluSerSerSerPheHisSerSer 359
DB 1015 TCTGTTCCACTGAGTGTGATGCTTCAAGTTTTCACCTCCAGC 1056

RESULT 4
AAH99952
ID AAH99952 standard; cDNA; 1059 BP.
XX
XX AAH99952;
AC 18-JUN-2002 (first entry)
XX
XX
DE CXCR4 encoding sequence.
XX
XX Human Chemokine receptor 4; CXCR4; gene; human; ss;
KW Chromosome 2q21; HIV-1.
XX
XX Homo sapiens.
OS
XX
XX Key
XX Location/Qualifiers
FT replacement (414,T)
FT /tag= a
FT /standard_name= "single nucleotide polymorphism"
FT replacement (783,T)
FT /tag= b
FT /standard_name= "single nucleotide polymorphism"

PA (KISH/) KISHIMOTO T.
 XX
 PI Kishimoto T, Nagasawa T, Tachibana K;
 XX
 DR WPI: 1999-591042/50.
 DR P-PSDB: AAY39933.
 XX
 PT Vascularisation inhibitors
 XX
 PS Disclosure: Page 48-49; 63pp; Japanese.
 XX
 CC This sequence encodes the human CXCR4 protein. The invention relates to
 CC remedies inhibiting neovascularisation, remedies for solid cancer,
 CC remedies for diseases pathologically caused by neovascularisation and
 CC tissue repairing agents containing as the active ingredient a substance
 CC capable of potentiating CXCR4. Based on a finding that vascularisation is
 CC inhibited in a CXCR4 knockout mouse, it becomes possible to prepare
 CC remedies inhibiting vascularisation which contain as the active
 CC ingredient a substance capable of potentiating CXCR4, remedies for solid
 CC cancer, remedies for diseases pathologically caused by neovascularisation
 CC and tissue repairing agents containing as the active ingredient a
 CC substance capable of potentiating CXCR4. It is also possible to establish
 CC methods for treatment with the use of these remedies.
 SQ Sequence 1588 BP; 396 A; 375 C; 334 G; 483 T; 0 other;

Alignment Scores:

Pred. No.: 3,366-187 Length: 1588
 Score: 1678.50 Matches: 319
 Percent Similarity: 95.48% Conservative: 19
 Best Local Similarity: 90.11% Mismatches: 11
 Query Match: 89.90% Indels: 5
 DB: 20 Gaps: 1

US-09-367-052-2 (1-359) x AA227610 (1-1588)

QY 6 ValSerIleTyrThrSerAspAsnTyrSerGluGluValGlySerGlyAspTyrAspSer 25
 DB 10 ATCAGTATATACACTTACAGTACAGTACACCGAGAAATGGGCTCAGGGGACTATGACTCC 69
 QY 26 AsnLysGluProCysPheArgAspGluAsnValHisPheAsnArgIlePheLeuProThr 45
 DB 70 ATGAAGGAACCTGTTCCGTGAGAAATGCTAATTTCAATAAATCTCTCGCCACC 129
 QY 46 IleTyrPheIleIlePheLeuThrGlyIleValGlyAsnGlyLeuValIleLeuValMet 65
 DB 130 ATCTACTCCATCATCTTCTTACTGCGCATGTGGCGAATGAGTGTGTCATCTGTGTCATG 189
 QY 66 GlyTyrGlnLysLysLeuArgSerMetThrAspLysTyrArgLeuHisLeuSerValAla 85
 DB 130 GGTACCAAGAAAGAACTGAGAGCATGACGAGACAGTACAGGCTGCACCTGCAGTGGCC 249
 QY 86 AspLeuLeuPheValIleThrLeuProPheThrAlaValAspAlaMetAlaAspTyrPyr 105
 DB 250 GACCTCTCTTGTATATACAGCTCTCTTGGGAGATTGATGCGGCAACAGTGTAC 309
 QY 106 PheGlyLysPheLeuCysLysAlaValHisIleIleTyrThrValAsnLeuTyrSerSer 125
 DB 310 TTGGGAACCTCTTGCAGAGCATGCTCATCTACACAGTCAACCTCTACAGCAGT 369
 QY 126 ValLeuIleLeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThrAsn 145
 DB 370 GTCCATACCTCGGCTTATAGTCTGACGCGCTACGCGCATGCTGCACGCCACAC 429
 QY 146 SerGlnArgProArgLysLeuLeuAlaGluLysAlaValTyrValGlyValTrpIlePro 165
 DB 430 AGTCAGAGGCCAAGAGAGCTGTGGCTGAAAAGGGGTCTATGTGGCGTGGATTCCT 489
 QY 166 AlaLeuLeuLeuThrIleProAspPheIlePheAlaAspValSerGlnGlyAspIleSer 185
 DB 490 GCCCTCTGCTGACTATTCGCCAGCTTCACTTTTGGCAAGCTC-----AGT 534
 QY 186 GlnGlyAspAspArgTyrIleCysAspArgLeuTyrProAspSerLeuTrpMetValVal 205

DB 535 GAGGACAGATGACAGATATATCTGTGACCGCTCTACCCCAATGACTTGGGTGGTTGTG 594
 QY 206 PheGlnPheGlnHisIleMetValGlyLeuIleLeuProGlyIleValIleLeuSerCys 225
 DB 595 TTCCAGATTTCACACATCATGCTTGGCCCTATCTGCGGTATGTGATCATCTCTGCTGC 654
 QY 226 TyrCysIleIleIleSerLysLeuSerHisSerLysGlnHisGlnLysArgLysAlaLeu 245
 DB 655 TATTCATATATCTCTCAAGCTGTACACTCCAGAGGCGCACAGAGCGCAGGCCCTTC 714
 QY 246 LysThrThrValIleLeuIleLeuAlaPhePheAlaCysTrpLeuProTyrTyrValGly 265
 DB 715 AAGACACAGATCATCTCTCTGCTTCTTCTGCTGTGGCTGCTTACTACTATGAG 774
 QY 266 IleSerIleAspSerPheIleLeuLeuGlyValIleLysGlnGlyCysAspPheLeuSer 285
 DB 775 ATCAGCATCGACTCTCTCTCTGAGAAATCAACAGCAAGGCTGTGAGTTTGAGAAC 834
 QY 286 IleValHisLysTrpIleSerIleThrGluAlaLeuAlaPheHisCysCysLeuAsn 305
 DB 835 ACTGTGCACAGTGAATTTCCATCACCGAGGCCCTAGCTTTCTTCCACTGTTGTGAGAC 894
 QY 306 ProIleLeuTyrAlaPheLeuGlyAlaLysPheLysSerSerAlaGlnHisAlaLeuAsn 325
 DB 895 CCCATCTCTATGCTTCTCTTCTGAGCCAAATTTAAACCTCTGCCACAGCACTACACC 954
 QY 326 SerMetSerArgGlySerSerLeuLysIleLeuSerLysGlyLysArgGlyHisSer 345
 DB 955 TCTGTGACAGAGGGTCCAGCCTCAAGATCTCTCTCAAGAGAAACCGAGGTGAGCATTTCA 1014
 QY 346 SerValSerThrGluSerCysLeuSerSerPheHisSerSer 359
 DB 1015 TCTGTTCCACTGAGCTTGAGTCTTCAAGTTTTCACCTCCAGC 1056

RESULT 6
 AAA61656
 ID AAA61656 standard; DNA; 1664 BP.
 XX
 AC AAA61656;
 XX
 DT 23-OCT-2000 (first entry)
 XX
 DE Human CXC chemokine receptor (CXCR4) cDNA.
 XX
 KW CXCR4: human CXC chemokine receptor 4; HIV infection inhibition;
 KW expression inhibition; antisense therapy; ss.
 XX
 OS Homo sapiens.
 OS
 PH Key Location/Qualifiers
 FT primer_bind 67..90
 FT /*tag= a
 FT /bound_moiety= "Antisense oligonucleotide SEQ ID NO:1
 FT (AAA61652)"
 FT primer_bind 73..96
 FT /*tag= b
 FT /bound_moiety= "Antisense oligonucleotide SEQ ID NO:2
 FT (AAA61653)"
 FT primer_bind 61..83
 FT /*tag= b
 FT /bound_moiety= "Antisense oligonucleotide SEQ ID NO:3
 FT (AAA61654)"
 XX
 PN WO200031271-A1.
 XX
 PD 02-JUN-2000.
 XX
 PE 24-NOV-1999; 99WO-JP06534.
 XX
 PR 24-NOV-1998; 98JP-0332760.
 XX
 PA (HISM) HISAMITSU PHARM CO LTD.

XX Iijima O, Goto T, Shimada T;
XX WPI: 2000-400081/34.
XX
XX Antisense oligonucleotide, useful as inhibitor in preventive or remedy
XX for HIV infection with high therapeutic efficacy
XX
XX Example 1; Page 17-18; 21pp; Japanese.
XX
XX The invention relates to human CXCR4 chemokine receptor 4 (CXCR4)-specific
XX antisense oligonucleotides (AA61652-A61654). The oligonucleotides
XX hybridise with the CXCR4 gene and/or CXCR4 RNA, thereby preventing its
XX expression. As CXCR4 plays a role in HIV infection, the antisense
XX oligonucleotides act as inhibitors of this process. Compositions
XX containing the antisense oligonucleotides are useful as prophylactic
XX or therapeutic agents for HIV infection. Such compositions are highly
XX efficacious for inhibiting infection with HIV. The present sequence
XX represents a human CXCR4 cDNA.

Sequence 1664 BP: 414 A; 398 C; 359 G; 493 T; 0 other;

Alignment Scores:

Score: No.:	3.6e-187	Length:	1664
Percent Similarity:	1678.50	Matches:	319
Best Local Similarity:	95.48%	Conservative:	19
Query Match:	90.11%	Mismatches:	11
	89.90%	Indels:	5
	21	Gaps:	1

US-09-367-052-2 (1-359) x AA61656 (1-1664)

QY 6 ValserIleYrThrSerAspAsnTyrSerGluGluValGlySerGlyAspTyrAspSer 25
Db ::
Db 86 ATCAGTATATACCTTACAGTAATACACCGAGCAATGGCTCAGGGGACTATGACTCC 145
QY 26 AsnLysGluProCysPheArgAspGluAsnValHisPheAsnArgIlePheLeuProThr 45
Db ::
Db 146 ATGAAGAACCCCTTTCCGTGAGAAATAATCTCAATTAATAATCTCTCCGCCACC 205
QY 46 IleYrPheIleIlePheLeuThrGlyTLeValGlnGlnGlyLeuValIleLeuValMet 65
Db ::
Db 206 ATCTACCTCATTACCTCTTAACTGCAATGCTGGCAATGATGATGCTCATCTGCTCATG 265
QY 66 GlyTyrGlnLysLysLeuArgSerMetThrAspLysTyrArgLeuHisLeuSerValAla 85
Db ::
Db 266 GGTACCAAGAAAGACAGAGCATGACGAGCAAGACAGAGCTGACCTGACGTGCC 325
QY 86 AspleuLeuPheValIleThrLeuProPheTrpAlaValAlaMetValAspTrpTyr 105
Db ::
Db 326 GACCTCCTTTGTCATCAGCGCTTCCCTTGGGCAAGTGTGCGGCAAACTGGTAC 385
QY 106 PheGlyLysPheLeuCysLysAlaValHisIleIleTyrThrValAsnLeuTyrSerSer 125
Db ::
Db 386 TTGTGGAACTTCCTATGCAAGAGCATGCTCATGCAACAGCAACCTCTACAGCAGT 445
QY 126 ValLeuIleLeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThrAsn 145
Db ::
Db 446 GTCCTCATCTCGGCTTCATGACTGTGACCGCTACCTGCGCATGCTCCACGCCAAC 505
QY 146 SerGlnArgProArgLysLeuLeuAlaGluLysAlaValTyrValGlyValTrpIlePro 165
Db ::
Db 506 AGTCAGAGGCCAAGAGAGCTGTGCTGAAGAGGTGCTGTGGGCTGTGATCCCT 565
QY 166 AlaLeuLeuLeuThrIleProAspPheIlePheAlaAspValSerGlnGlyAspIleSer 185
Db ::
Db 566 GCCCTCCTGCTGACTATTCGCGACTTCATCTTCCCAACGCTC-----AGT 610
QY 186 GlnGlyAspAspArgTyrIleCysAspArgLeuTyrProAspSerLeuTrpMetValVal 205
Db ::
Db 611 GAGGCAAGTGAACATATATCTGTGACCGCTTCTACCCCAATGACTTGTGGTGTGTG 670
QY 206 PheGlnPheGlnHisIleMetValGlyLeuLeuLeuProGlyIleValIleLeuSerCys 225

Db 671 TTCAGTTTCAGCAGCATGATGCTGGCTTATCCTGCTGATGTCATCTCTGCTGC 730
QY 226 TyrCysIleIleIleSerLysLeuSerHisSerLysGlnLysArgLysAlaLeu 245
Db 731 TATTCATTTATCATCTCCAAAGCTGTCACACTCCAAAGGCCACCAAGGCCAACGCCCTC 790
QY 246 LysThrThrValIleLeuAlaPhePheAlaPhePheAlaCysTrpLeuProTyrTyrValGly 265
Db 791 AAGACACAGTCATCTCATCTGCTGCTTTCTTCCCTGCTTGGCTGCTTACTACATTGGG 850
QY 266 IleSerIleAspSerPheIleLeuLeuGlyValIleLysGlnGlyCysAspPheGluSer 285
Db 851 ATCAGCATCGACCTCTCATCTCTCTGGAATCATCAAGCAAGGGTGTGAGATTGAGAAC 910
QY 286 IleValHisLysTrpIleSerIleThrGluAlaLeuAlaPhePheHisCysLysLeuAsn 305
Db 911 ACTGTGACACAGTGAATTCATCTACCGAGGCCCTTACTCTTCTTCCACTGTGTCTGAC 970
QY 306 ProIleLeuTyrAlaPheLeuGlyAlaLysPheLysSerSerAlaGlnHisAlaLeuAsn 325
Db 971 CCCATCCTCTATGCTTTCCCTTGGAGCAATTTAAACCTCTGCCACGACGACTCACC 1030
QY 326 SerMetSerArgLysSerSerLeuLysIleLeuSerLysGlyLysArgLysHisSer 345
Db 1031 TCTGTGACAGAGAGGCTCAGCCTCAAGATCCTCTCCAAAGCAAGGAGGTGACATTCA 1090
QY 346 SerValSerThrGluSerGluSerSerSerPheHisSerSer 359
Db 1091 TCTGTTCACCTGAGTCTGAGCTTTCAAAGTTTTCATCTCCACG 1132

RESULT 7

AAZ40014
ID AAZ40014 standard; DNA; 1664 BP.

AC AAZ40014;

AC 14-FEB-2000 (first entry)

DE CXCR4 coding sequence.

KW CXCR4; inhibitor; antisense oligonucleotide; anti-HIV agent;

KW HIV infection; therapy; ss.

XX Synthetic.

XX Jp11285391-A.

XX 19-OCT-1999.

XX 18-NOV-1998; 98JP-0327942.

XX 19-NOV-1997; 97JP-0335085.

XX (HISM) HISAMITSU PHARM CO LTD.

XX (TOAG) TOA GOSSEI CHEM IND LTD.

XX WPI: 2000-026817/03.

XX An oligonucleotide used as an anti-HIV agent - inhibits CXCR4 protein

XX expression

XX Disclosure; Page 5-6; 6pp; Japanese.

XX This sequence represents a CXCR4 coding sequence. The invention relates

XX to antisense oligonucleotides that hybridise specifically with

XX chromosomal DNA and/or RNA encoding a CXCR4 protein, and inhibit the

XX expression of the CXCR4 protein. The antisense oligonucleotides can be

XX used in an anti-HIV agent. The oligonucleotides and the anti-HIV agent

XX are highly effective as a preventive and treating agent for HIV

XX infection.

XX Sequence 1664 BP: 414 A; 398 C; 359 G; 493 T; 0 other;

Alignment Scores:

Pred. No.: 3,66-187 Length: 1664
 Score: 1678.50 Matches: 319
 Percent Similarity: 95.48% Conservative: 19
 Best Local Similarity: 90.11% Mismatches: 11
 Query Match: 89.90% Indels: 1
 Gaps: 21

US-09-367-052-2 (1-359) x AA240014 (1-1664)

```

OY 6 ValSerIleYrThrSerAspAsnTyrSerClnuValGlySerGlyAspTyrAspSer 25
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 86 ATCAGTATATACACTGATGATACACACGAGAAATGGCTCAGGGAGTATGACTCC 145
OY 26 AsnIysGluProCysPheArgSPGLAsnValHisPheAsnAqIlePheLeuProThr 45
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 146 ATGAGAGAACCTCTTCCGGAAGAAATGCTTAATTCATTAATAATCTTCTCCACC 205
OY 46 IleTyrPheIleIlePheLeuThrGlyIleValGlyAsnGlyLeuValIleLeuValMet 65
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 206 ATCTACATCATCATCTTCTTAAGTGGCATGTGGCAATGGATGGTGCATCTGTCATG 265
OY 66 GlyTyrGlnLysLysLeuArgSerMetThrAspLysTyrArgLeuHisLeuSerValAla 85
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 266 GGTACACAGAGAAACAGACGATGACGACAGCAAGTACAGGGCTGCACCTGCAGTGGCC 325
OY 86 AspleuLeuPheValIleThrLeuProPheThrAlaValAspAlaMetAlaAspTyrTyr 105
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 326 GACCTCCTCTTGTGATCAGCAGCTTCCCTCTGGGCACTGATGCGCGCAACTGGTAC 385
OY 106 PheGlyLysPheLeuCysLysAlaValHisIleIleTyrThrValAsnLeuTyrSerSer 125
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 386 TTGTGGAACTTCCATGCAAGGCGAGTCCATGCTACACAGCAACCTCTACAGCAGT 445
OY 126 ValLeuLeuLeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThrAsn 145
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 446 GTCTCATCTCGGCTTCATGCTGACCGCTTACCTGGCCATGTCACGACGACGAC 505
OY 146 SerGlnArgProArgLysLeuAlaGlnLysAlaValTyrValGlyValTyrPrlPro 165
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 506 AGTCAGAGGCCAAGAGAGCTTGTGGTGAAGAGTGTCTATGTGGCGTGTGATCCCT 565
OY 166 AlaLeuLeuLeuThrIleProAspPheIlePheAlaAspValSerGlnGlyAspIleSer 185
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 566 GCCCTCTCGTGAATATCCGCACTTCTTCCCAAGC-----AGT 610
OY 186 GlnGlyAspAspArgTyrIleCysAspArgLeuTyrProAspSerLeuTyrPrlMetVal 205
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 611 GAGGCAATGACAGATATATCTGTGACCGCTTACCCCAATGACTTGTGGTGTG 670
OY 206 PheGlnPheGlnHisIleMetValGlyLeuLeuLeuProGlyIleValIleLeuSerCys 225
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 671 TTCAGTTCAGCAATCATGTTGGCTTATCTGCTGATGTTCATCTCTCTCTC 730
OY 226 TyrCysIleIleIleSerLysLeuSerHisSerLysGlnGlnLysArgLysAlaLeu 245
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 731 TATTCATTTATCATCTCAGAGCTGCACACCTCAAGGCGCCACGAGAGCGAGCCCTC 790
OY 246 LysThrThrValIleLeuIleLeuAlaPhePheIleCysTyrPrlLeuProTyrValGly 265
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 791 AAGGCCACAGTATCTCATCTGCTTCTTCCCTGTGGCGCTTACTATCATATGGG 850
OY 266 IleSerIleAspSerPheIleLeuLeuGlyValIleLysGlnGlnCysAspPheGlnSer 285
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 851 ATCAGCATCAGCTCTTCATCTCTCTGGAATCATCAAGCAGAGGTGTGAGTTGAC 910
OY 286 IleValHisLysTyrPrlSerIleThrGlnAlaLeuAlaPhePheHisCysCysLeuAsn 305
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 911 ACTGTGCACAGTGTGATTTCCATCAGGAGCCCTTACTTCTTCCACTGTGTGCTAAC 970
OY 306 ProlLeuTyrAlaPheLeuGlyAlaLysPheLysSerSerAlaGlnHisAlaLeuAsn 325
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
  
```

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Db 971 CCATCTCTATGCTTCTTGGAGCCAAATTAACCTCTGCCCCAGCAGCATTCACC 1030
OY 326 SerMetSerArgGlySerSerLeuLysIleLeuSerLysGlyLysArgGlyLysSer 345
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 1031 TCTGTGACAGAGGGTCCACCTCTCAATCTCTCCAAAGAAAGCAGAGTGCACATTC 1090
OY 346 SerValSerThrGlnSerGlnSerSerPheHisSerSer 359
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 1091 TCTGTTCACACTGACTGCTCTTCAAGTTTTCATCTCAGC 1132
RESULT 8
ABK83803 standard; cDNA; 1670 bp.
ID ABK83803
XX
AC ABK83803:
XX
DT 14-Aug-2002 (first entry)
XX
DE Human cDNA differentially expressed in granulocytic cells #374.
XX
KW Human; ss; granulocytic cell; DNA chip; bacterial infection;
KW viral infection; parasitic infection; protozoal infection;
KW fungal infection; sterile inflammatory disease; psoriasis;
KW rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;
KW cardiac reperfusion injury; renal reperfusion injury; ARDS;
KW adult respiratory distress syndrome; inflammatory bowel disease;
KW Crohn's disease; ulcerative colitis; peridominal disease;
KW granulocyte activation; chronic inflammation; allergy.
XX
OS Homo sapiens.
XX
PN W0200228999-A2.
XX
PD 11-Apr-2002.
XX
PE 03-Oct-2001; 2001MO-US10821.
XX
PR 03-Oct-2000; 2000US-237189P.
XX
PA (GENE-) GENE LOGIC INC.
XX
PI Beezer-Barclay Y, Weissman SM, Yamaga S, Vockley J;
XX
DR WPI: 2002-435328/46.
XX
PT Detecting granulocyte activation by detecting differential expression
PT of genes associated with granulocyte activation, which serves as
PT diagnostic markers that is useful for monitoring disease states and
PT drug toxicity
XX
PS Claim 1; SEQ ID NO 374; 114bp; English.
XX
CC The invention relates to detecting (M1) granulocyte (GC) activation
CC (GCA), by detecting the level of expression of gene(s) (Gs) identified by
CC DNA chip analysis as given in the specification, and comparing
CC the expression level to an expression level in an unactivated
CC GC, where differential expression of Gs is indicative of GCA.
CC Also included are modulating (M2) GA by contacting GC with an agent
CC that alters the expression of at least one gene in Gs; (2) screening (M3)
CC for an agent capable of modulating GCA or an inflammation (especially
CC chronic) in a tissue, an allergic response in a subject, exposure of a
CC subject to a pathogen or sterile inflammatory disease using the
CC gene expression profile; (3) detecting (M4) an inflammation (especially
CC chronic) in a tissue, an allergic response in a subject, exposure of a
CC subject to a pathogen or sterile inflammatory disease, by detecting the
CC level of expression in a sample of the tissue of gene(s) from Gs, where
CC the level of expression of the gene is indicative of inflammation;
CC (4) treating (M5) an inflammation (especially chronic) or in a tissue,
CC an allergic response in a subject, exposure of a subject to a pathogen
CC or sterile inflammatory disease, by contacting a tissue having
CC inflammation with an agent that modulates the expression of gene(s)
CC from Gs in the tissue. M1 is useful for detecting GCA; M2 is useful for
CC modulating GA; M3 is useful for screening an agent capable of modulating
  
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CC GCA preferably in an inflammation in a tissue; M4 is useful for
 CC detecting an inflammation (especially chronic) in a tissue, an allergic
 CC response in a subject, exposure of a subject to a pathogen or sterile
 CC inflammatory disease (e.g. psoriasis, rheumatoid arthritis,
 CC glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal
 CC reperfusion injury, AKOs, adult respiratory distress syndrome,
 CC inflammatory bowel disease, Crohn's disease, ulcerative colitis,
 CC periodontal disease; also bacterial infection, viral infection,
 CC parasitic infection, protozoal infection, fungal infection and M5 is
 CC useful for treating one of the above conditions. The present
 CC sequence represents a gene differentially expressed in granulocytes.
 CC Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic
 CC format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 1670 BP: 418 A: 400 C: 361 G: 491 T: 0 other:

Alignment Scores:

No.:	3.62e-187	Length:	1670
Present Similarity:	1678.50	Matches:	319
Best Local Similarity:	95.48%	Conservative:	19
Query Match:	89.11%	Mismatches:	11
	24	Gaps:	5
			1

US-09-367-052-2 (1-359) x ABK83803 (1-1670)

OY 6 ValSerIleTyrThrSerAspAsnTyrSerGluGluValGlySerGlyAspTyrAspSer 25
 DB 82 ATCAGTATATACCTTCAGTACACTACACCGAGAAAGGGCTCAGGGAGCTATGACACC 141
 OY 26 AsnLysGluProCysPheArgAspGluAsnValHisPheAsnArgIlePheLeuProThr 45
 DB 142 ATGAGAGAACCTGTTCCGTGAGAGAAATGCTAATTCATTAATATCTTCCGCCACC 201
 OY 46 IleTyrPheIleIlePheLeuThrGlyIleValGlyAsnGlyLeuValIleLeuValMet 65
 DB 202 ATCTACCTCATCATCTTCTTAAGTCGCATGTGGGCATGATGATGTCATCCTGTCATG 261
 OY 66 GlyTyrGlnLysLysLeuArgSerMetThrAspLysTyrArgLeuHisLeuSerValAla 85
 DB 262 GGTACCAAGAAAGAACTAGAGACATGACGAGCAAGTACAGCTGCACCTGCACCTGCC 321
 OY 86 AspleuLeuPheValIleThrLeuProPheThrPalaValAspAlaMetAspTyrTyr 105
 DB 322 GACCTCCTTGTTCATACGCTTCCCTTGGGAGTGGATGCCGCAACCTGGTAC 381
 OY 106 PheGlyLysPheLeuCysLysAlaValHisIleIleTyrThrValAsnLeuTyrSerSer 125
 DB 382 TTGGGAACTTCCTATGCAAGGAGTCATCATCTACACAGTCACCTGTACAGCAGT 441
 OY 126 ValLeuIleLeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThrAsn 145
 DB 442 GTCCCTACCTCGGCTTCATAGCTGAGCGCTACCTGCGCATCGTCACGCCACAC 501
 OY 146 SerGlnArgProArgLysLeuLeuAlaGlyLysAlaValTyrValGlyValTyrIlePro 165
 DB 502 AGTCAGAGGCCAAGAAAGCTGTGGCTGAAGAGGCTGTATGTTGGCTGTGATCCCT 561
 OY 166 AlaLeuLeuLeuThrIleProAspPheIlePheAlaAspValSerGlnGlyAspIleSer 185
 DB 562 GCCCTCCGTGACATATCCGACATCTCATCTTGGCAACGTC-----AGT 606
 OY 186 GlnGlyAspAspArgTyrIleCysAspArgLeuTyrProAspSerLeuTyrMetValVal 205
 DB 607 GAGGAGATGACAGATATATGTGACCGCTTCAACCCAAATGACTTGTGGGTGTGTG 666
 OY 206 PheGlnPheGlnHisIleMetValGlyLeuLeuLeuProGlyIleValIleLeuSerCys 225
 DB 667 TTCAGTTTACGACATATGATGTTGGCTTATCCGCTGTATGATGATCTGTGCTGCC 726
 OY 226 TyrCysIleIleIleSerLysLeuSerHisSerLysGlnHisGlnLysArgLysAlaLeu 245

DB 727 TATTCATTATCATCTCCAAAGCTGTACACATCCAAAGGCCACCAAGCGCAGCCCTC 786
 OY 246 LysThrThrValIleLeuIleLeuAlaPhePheAlaCysTyrPleuProTyrTyrValGly 265
 DB 787 AAGACCAAGATCATCTCATCTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTG 846
 OY 266 IleSerIleAspSerPheIleLeuLeuGlyValIleLysGlnGlyCysAspPheGluSer 285
 DB 847 ATCAGATTCGACTCTTCTATCTCTCTGGAATATCATCAAGAGGCTGTGAGTTTACAGAC 906
 OY 286 IleValHisLysTyrPleuSerIleThrGluAlaLeuAlaPhePheHisCysCysLeuAsn 305
 DB 907 ACTGTCACAGATGATTCATCATCAGGAGGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTG 966
 OY 306 ProIleLeuTyrAlaPheLeuGlyValLysPheLysSerSerAlaGlnHisAlaLeuAsn 325
 DB 967 CCCATCCCTATATGCTTCTTGTGAGCCAAATTTAAACCTGTGCCACAGCAGCTACCC 1026
 OY 326 SerMetSerArgGlySerSerLeuLysIleLeuSerLysGlyLysArgGlyGlyHisSer 345
 DB 1027 TCTGTGACAGAGGCTCCAGCTTCAAGATCTCTCTCAAGAAAGCGAGGTGACATTCA 1086
 OY 346 SerValSerThrGluSerGluSerSerSerPheHisSerSer 359
 DB 1087 TCTGTTCACAGTGTGAGTCTTCAAGTTTTCACCTCCAGC 1128

RESULT 9

ABN95645 standard; DNA: 1670 BP.

ABN95645;

13-AUG-2002 (first entry)

Gene #2143 used to diagnose liver cancer.

Gene: liver cancer; ds: hepatocellular carcinoma; hepatotropic;
 metastatic liver tumour; cytostatic; expression profile; disease state;
 disease progression; drug toxicity; drug efficacy; drug metabolism.

Homo sapiens.

WO200229103-A2.

11-APR-2002.

02-OCT-2001; 2001WO-US30589.

02-OCT-2000; 2000US-237054P.

(GENE-) GENE LOGIC INC.

Horne D, Alvares C, Peres-Da-Silva S, Vockley JG;

WPI: 2002-426119/45.

Diagnosing and detecting the progression of liver cancer,
 hepatocellular carcinoma or metastatic liver tumor in a patient,
 involves detecting the level of expression of two or more genes in a
 liver tissue sample

Claim 1; SEQ ID NO 2143; 298bp; English.

The invention relates to a novel method for diagnosing and detecting the
 progression of liver cancer, hepatocellular carcinoma or metastatic liver
 tumor in a patient, and differentiating metastatic liver cancer from
 hepatocellular carcinoma in a patient, involving detecting the level of
 expression of two or more genes represented in ABN933503-ABN97455 in a
 tissue sample. The method of the invention has hepatotropic, and
 cytostatic activity. The method is useful for diagnosing and detecting
 the progression of liver cancer, hepatocellular carcinoma and metastatic
 liver carcinoma in a patient. The method is useful for identifying

expression profiles which serve as useful diagnostic markers as well as markers that can be used to monitor disease states, disease progression, drug toxicity, drug efficacy and drug metabolism.
CC Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/publ/seqs-sequences.

SO Sequence 1670 BP; 418 A; 400 C; 361 G; 491 T; 0 other:

Alignment Scores:

Pred. No.:	3.62e-187	Length:	1670
Score:	1678.50	Matches:	319
Percent Similarity:	95.48%	Conservative:	19
Best Local Similarity:	90.11%	Mismatches:	11
Query Match:	89.90%	Indels:	5
DB:	24	Gaps:	1

US-09-367-052-2 (1-359) x ABN95645 (1-1670)

```
6 ValSerIleTyrrThrSerAspAsnTyrrSerGluGluValGlySerGlyAspTyrrAspSer 25
82 ATCAGTATATACCTTTCAGATTAACACCGAGAAATGGCTCGGGGAGCTATGACTCC 141
26 AsnIlysgIuproCysPheArGAspGluAsnValHisPheAsnArGlyIlePheLeuProthr 45
142 ATGAGAGAACCTGTTTCGTGAGAAATGCTATATTCAATAAATCTTCTGCGCCACC 201
46 IleTyrrPheIleIlePheLeuThrGlyIleValGlyAsnGlyLeuValIleLeuValMet 65
202 ATCTACTCCATCACTCTTCTTAACGTGGCATTTGGGCAATGGATGGTCACTCTGTCATG 261
66 GlyTyrrGlnIlySlyLeuArGSerMetThrAspIlyTyrrArGlyLeuHisLeuSerValAla 85
262 GGTACACGAGAAAGAACTGAGAAAGCATGACGAGCAAGTACAGGCTCCACCTGCACTGCC 321
86 AspleuLeuPheValIleThrLeuProPheTrpAlaValAspAlaMetAlaAspTrpTyrr 105
322 GACCTCCTTGTTCATCAGCTTCCCTTGTGGGAGATGATGCGCGCAACCTGGGTAC 381
106 PheGlyIlySlyPheLeuCysIlyAlaValHisIleIleTyrrThrValAsnLeuTyrrSer 125
382 TTTGGGAACCTTCATGACAGGCACTGCTCATCTACACAGTCAACCTCTACAGCAGT 441
126 ValLeuIleLeuAlaPheIleSerLeuAspArGlyTyrrLeuAlaIleValHisAlaThrAsn 145
442 GTCTCATCTCGGCTTATCATGCTGACCGCTACCTGCGCATGCTCCAGCCGCCAC 501
146 SerGlnArGProArGlySlyLeuAlaGluIlyAlaValTyrrValGlyValTrpIlePro 165
502 AGTCAGAGCCAGAGAACTGTTGGCTGAAAAGGTGCTCATGTTGGGCTGGATCCCT 561
166 AlaIleuLeuLeuThrIleProAspPheIlePheAlaAspValSerGlnGlyAspIleSer 185
562 GCCCTCCGCGACATATCCGACATTCATCTTGGCAACGTC-----AGT 606
186 GlnGlyAspAspArGlyTyrrIleCysAspArGlyLeuTyrrProAspSerLeuTrpMetValAla 205
607 GAGCAGATGACAGATATATCTGACCGCTTTCACCCCAATGACTTGGGTGGTGTG 666
206 PheGlnPheGlnHisIleMetValGlyLeuIleLeuProGlyIleValIleLeuSerCys 225
667 TTCAGTTTGACACATCATGTTGGCTTATCCGCTGATGATGATGATGATGATGATGATG 726
226 TyrrCysIleIleIleSerIlySlyLeuSerHisSerIlyGlnHisGlnIlyArGlyAlaLeu 245
727 TATTGCATATATCACTCCAGACTGTCACATCCAGAGGCCACCGAAGGCCCTTC 786
246 LysThrTrpValIleLeuIleLeuAlaPhePheAlaCysTrpLeuProTyrrTyrrValIly 265
787 AAGACACAGCATCTCATCTGCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 846
266 IleSerIleAspSerPheIleLeuGluGlyIleIlySlyGlnIlyCysAspPheGluSer 285
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DB 847 ATCAGATCAGACTCCTTCATCTCCTCGAATCATCAAGCAAGGCTGAGCTTGAGAAC 906
QY 286 IleValHisIlyTrpIleSerIleThrGluAlaLeuAlaPhePheHisCysCysLeuAsn 305
DB 907 ACTGGCAGCAAGTGGATTTCATCACCAGGCGCCCTAGCTTCTTCTCCTGCTGTAAC 966
QY 306 ProIleLeuTyrrAlaPheLeuGlyAlaIlySlyPheIlySerSerAlaGlnHisAlaLeuAsn 325
DB 967 CCCATCTCTATGCTTCTTCTTCTGACGCCAAATTTAAACCTCTGCCACAGCAGCTGACC 1026
QY 326 SerMetSerArGlySerSerLeuIlySlyLeuSerIlyGlyArGlyGlyHisSer 345
DB 1027 TCTGAGACAGAGGATCCAGCCTCAAGATCTCTCCAAAGGAAAGCGAGTGGACATTTCA 1086
QY 346 SerValSerThrGlnIlySerGlnIlySerSerPheHisSerSer 359
DB 1087 TCTGTTCCACTGAGTGTGAGTCTTCAAGTTTCACTCCAGC 1128

RESULT 10
AA165467
ID AA165467 standard; DNA; 1679 BP.
XX
AC AA165467;
XX
DF 10-DEC-2001 (first entry)
XX
DE Nucleotide sequence of a human polynucleotide.
XX
KW Human; receptor; DC-SIGN; dendritic cell; T lymphocyte; HIV;
KM gp120; C-type lectin; ICAM3; HIV entry; T cell; macrophage;
KN HIV infection; ss.
XX
OS Homo sapiens.
XX
PN WO200164752-A2.
XX
PD 07-SEP-2001.
XX
PF 28-FEB-2001; 2001WO-US06322.
XX
PR 02-MAR-2000; 2000US-0517605.
XX
PA (UYNV) UNIV NEW YORK STATE.
XX
PA (UYNV-) UNIV NIJMEGEN.
XX
PI Littman DR, Kwon D, Van Kooyk Y, Geijtenbeek T;
XX
DR WPI; 2001-602565/68.
XX
PT An antibody for the treatment or prevention of HIV-infection comprises
PT a gp120 portion which binds to DC-SIGN or is exposed upon gp120 binding
PT of DC-SIGN due to concomitant conformational change -
XX
PS Disclosure; Page 126-127; 131pp; English.
XX
CC The specification describes an antibody which is specific for an
CC antigenic fragment of gp120. This antigenic fragment binds to DC-SIGN
CC or is exposed upon gp120 binding of DC-SIGN due to concomitant
CC conformational change. DC-SIGN is a receptor that is specifically
CC expressed on dendritic cells and facilitates infection of T lymphocytes
CC with HIV. DC-SIGN is identical to a HIV-1 gp120-binding C-type lectin.
CC DC-SIGN binds ICAM-3 (which is expressed constitutively on T lymphocytes)
CC with high affinity. The antibody of the invention inhibits the trans
CC enhancement of HIV entry into a T cell or macrophage facilitated by
CC dendritic cells. The antibody is useful to treat or prevent HIV
CC infection. The present sequence represents a human polynucleotide,
CC which is used in the course of the invention.
XX
SQ Sequence 1679 BP; 407 A; 400 C; 368 G; 504 T; 0 other:
```

Alignment Scores:

Pred. No.:	3.65e-187	Length:	1679
Score:	1678.50 <td>Matches:</td> <td>319</td>	Matches:	319

US-09-367-052-2 (1-359) x AAD12801 (1-1679)

```

OY 6 ValSerIleThrPheSerAspSerGluGluValGlySerGlyAspTyrAspSer 25
DB 98 ATCAGTATATACACTTACATACAGGAAATGGCTCAGGGGACTATGACTCC 157
OY 26 AsnLysGluProCysPheArgAspGluAsnValHisPheAsnArgIlePheLeuProThr 45
DB 158 ATGAGGAGAACCCGTTTCCGTGAAGAAATGCTAATTTCAATAAATCTTCCTGCCACC 217
OY 46 IleTyrPheIleIlePheLeuThrGlyIleValGlyAsnGlyLeuValIleLeuValMet 65
DB 218 ATCACTACCATCACTCTTAACTGAGCATTTGGGCAATGGATGGATCACTGCTCATG 277
OY 66 GlyTyrGlnLysLeuArgSerMetThrAspLysTyrArgLeuHisLeuSerValAla 85
DB 278 GGTACCAAGAAAGAACTGAGAGACATGACGACAGGCTGACCTGCTGCTGCTGCC 337
OY 86 AspLeuDeuPheValIleThrLeuProPheTrpAlaValAspAlaMetAlaAspTrpTyr 105
DB 338 GACCTCCTCTTTGTCATCAGCGTCCCTCTGGGCAATGATGGCCGCAACTGGTAC 397
OY 106 PheGlyLysPheLeuGlyLysAlaValHisIleIleTyrThrValAsnLeuTyrSerSer 125
DB 398 TTTGGGAACTCTCATGCAAGGACATCATCATACAGTCAACCTCTACAGCAGT 457
OY 126 ValLeuIleLeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThrAsn 145
DB 458 GTCTCTCTCTGGCTTCATCATGCTGACCGCTACCTGGCATCGTCCAGCCAGCAC 517
OY 146 SerGlnArgProArgLysLeuLeuAlaGluLysAlaValTyrValGlyValTrpIlePro 165
DB 518 AGTCAGAGGCCAAGAAAGCTGTGGTGAAGAAGTGCTATGTTGGCGTGGATCCCT 577
OY 166 AlaLeuLeuLeuThrIleProAspPheIlePheAlaAspValSerGlnGlyAspIleSer 185
DB 578 GCCCTCCTGCTGATATCCGACCTCATCTTCCCAACGTC-----AGT 622
OY 186 GlnGlyAspAspArgTyrIleGlyAspArgLeuTyrProAspSerLeuTrpMetValVal 205
DB 623 GAGCAGATACAGCATATATCTGTGACCGCTTACCCCAATGACTGTGGTGGTGTG 682
OY 206 PheGlnPheGlnHisIleMetValGlyLeuIleLeuProGlyIleValIleLeuSerCys 225
DB 683 TTCCAGTTTACAGCATCATGATGTTGGCTTATCCTCGCTGATTCATCTGCTGCTGC 742
OY 226 TyrCysIleIleIleSerLysLeuSerHisSerLysGlyHisGlnLysArgLysAlaLeu 245
DB 743 TATTGCAATTATCTCTCAAGCTGTCACTCCAAAGGCCACAGAGCCCAAGGCCCTC 802
OY 246 LysThrThrValIleLeuIleLeuAlaPhePheAlaCysTrpLeuProTyrTyrValGly 265
DB 803 AAGACCAACATCATCCCATCTGCTGCTTCTTGCCCTGGTGGCTTCTCATTTGGG 862
OY 266 IleSerIleAspSerPheIleLeuLeuGlyValIleLysGlnGlyCysAspPheGluSer 285
DB 863 ATCAGCATCAGCTCTTCATCTCTGGAATATCATCAAGAGGCTGAGTTTGAAGAAC 922
OY 286 IleValHisLysTrpIleSerIleThrGluAlaLeuAlaPhePheHisCysCysLeuAsn 305
DB 923 ACTGTGACAAAGGATTTCCATCCAGGAGCCCTTCTTCCACTGTTTCGTGAAC 982
OY 306 ProIleLeuTyrAlaPheLeuGlyAlaValPheLysSerSerIleGlnHisAlaLeuAsn 325
DB 983 CCCATCCTCTATGCTTTCTTGAGACCAAAATTTAAATCTCTGCCAGCAGCACTCACC 1042
OY 326 SerMetSerArgLysSerSerLeuLysIleLeuSerLysGlyLysArgGlyGlyHisSer 345
DB 1043 TCTGTGAGCAGAGGCTCAGCCTCAAGATCTCTCCAAAGAAAGGAGGTGACATTTCA 1102
OY 346 SerValSerThrGluSerGluSerSerPheHisSerSer 359

```

```

DB 1103 TCTGTTTCACAGTGTGAGTCTTCAAGTTTTCACCTCAGC 1144
RESULT 12
AA080521
ID AA080521 standard; cDNA: 1737 BP.
XX
AC AA080521;
XX
DE 18-JUL-1995 (first entry)
XX
XX Human monocyte PF4AR cDNA.
XX
KW Interleukin-8 receptor; IL-8 receptor; PF4AR;
KW platelet factor superfamily receptor; monocyte; chemotactic;
KW inflammation; inflammatory disease; arthritis; emphysema; cystic;
KW fibrosis; colitis; bronchitis; meningitis; therapeutic; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 91..1149
FT     /*tag= a
XX
XX W09428931-A.
XX
XX 22-DEC-1994.
XX
XX 07-JUN-1994: 94WO-US06380.
XX
XX 11-JUN-1993: 93US-0076093.
XX
XX (GETH ) GENENTECH INC.
XX
XX Chuntharapal A, Hebert C, Kim KJ, Lee J;
XX
XX WPI, 1995-036114/05.
XX
XX DR P-PSDB: AAR68812.
XX
XX PT Treatment of inflammatory disorders - by administering an
XX antibody capable of binding a platelet factor 4 superfamily
XX receptor polypeptide
XX
XX PS Disclosure: Page 54-56: 83pp; English.
XX
XX 2 PF4AR members were identified by probing lambda libraries from
XX human monocyte-like cell line HL-60 and human peripheral blood
XX lymphocytes using a large fragment of IL-8 receptor DNA (full
XX sequence given in AA080520). The nucleotide sequences of the 2
XX PF4ARs are given in AA080521 and AA080522, and their respective
XX amino acid sequences in AAR68812 and AAR68813.
XX
SQ Sequence 1737 BP; 454 A; 411 C; 373 G; 499 T; 0 other;
Alignment Scores:
Pred. No.: 3.84e-187 Length: 1737
Score: 1678.50 Matches: 319
Percent Similarity: 95.48% Conservative: 19
Best Local Similarity: 90.11% Mismatches: 11
Query Match: 89.90% Indels: 5
DB: 16 Gaps: 1
US-09-367-052-2 (1-359) x AA080521 (1-1737)
OY 6 ValSerIleThrPheSerAspSerGluGluValGlySerGlyAspTyrAspSer 25
DB 100 ATCAGTATATACACTTACATACAGGAAATGGCTCAGGGGACTATGACTCC 159
OY 26 AsnLysGluProCysPheArgAspGluAsnValHisPheAsnArgIlePheLeuProThr 45
DB 160 ATGAGGAGAACCCGTTTCCGTGAAGAAATGCTAATTTCAATAAATCTTCCTGCCACC 219
OY 46 IleTyrPheIleIlePheLeuThrGlyIleValGlyAsnGlyLeuValIleLeuValMet 65

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Db      220 ATCTACTCATCATCTTCTTAACGTGGCAATGTGGCAATGGATGGTCACTCTGTCATG 219
OY      66  GATYTGILNLSYLSLEUARGSERMETTHRASPPLYSTYRARGHLSLEUSERVALA 85
        |||
Db      280 GGTACCAAGAACTGAGAACATGACGACGACAACTACAGGCTGCACTGTCAGTGCC 339
OY      86  ASPLLEUAPHEVALIETHRLEUPROPHETRPALAVASPALAMETALAASPTPTYR 105
        |||
Db      340 GACCTCTCTTTGTTCATCAGGCTTCCCTCTGCGAGTGTGATGCGCGCAACCTGATAC 399
OY      106 PHEGILYSPHELEUCYSLSYLSAVALHLSLEIETRYTHVALASNEUTYRSESR 125
        |||
Db      400 TTGGGAACTTCTTATGCAAGGACATGTCATCTACACACTCAACCTCTACACAGT 459
OY      126 VALLEUILEUAPHEVALIETHRLEUPROPHETRPALAVASPALAMETALAASPTPTYR 145
        |||
Db      460 GTCTCTATCTGCGCTTCTCATCTGACGTGGACGCTGACGCTGACGCTGACGCTGAC 519
OY      146 SERGLNARGPROARGYLSLEUVALAGLULYSALAVATYRVALGYALTYRPILEPRO 165
        |||
Db      520 AGTCAGAGGCGCAGAGAGCTGTGGCTGAAGAGTGTGATCTTGGCGCTGATCCCT 579
OY      166 ALALEUULEUTHRLIETHRLEUPROPHETRPALAVASPALAMETALAASPTPTYR 185
        |||
Db      580 GCGCTCTCTGCTGCTATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 624
OY      186 GLNGLYASPARPARGYRILECYASPARPARGYRILECYASPARPARGYRILECYAS 205
        |||
Db      625 GAGGCAAGATGACGATATATCTGTGACCGCTTACCCCAATCACTGTGGGTGGTGG 664
OY      206 PHEGLNPHGLNHSILEMETVALGLYLEUILEUPROGLYLEUILEUILEUSERCYS 225
        |||
Db      685 TTCACATTCAGACATCATCATGCTGGCTTATCTGCTGCTGCTGCTGCTGCTGCTGCT 744
OY      226 TYRCYSILLEIETHRLEUARGSERMETTHRASPPLYSTYRARGHLSLEUSERVALA 245
        |||
Db      745 TATTTGATATATCATCTCCAGCTGTACACTCCAGGCGCACCAAGGCGCACCAAGG 804
OY      246 LYSTHTRVALIETHRLEUVALIETHRLEUVALIETHRLEUVALIETHRLEUVALI 265
        |||
Db      805 AATACACAGTCTCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 864
OY      266 ILESERILEASPERPHEILEUVALIETHRLEUVALIETHRLEUVALIETHRLEU 285
        |||
Db      865 ATCAGCATGACCTCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 924
OY      286 ILEVALHLSYLSLEUARGSERMETTHRASPPLYSTYRARGHLSLEUSERVALA 305
        |||
Db      925 ACTGTGCAAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 984
OY      306 PROILEUETHRLEUVALIETHRLEUVALIETHRLEUVALIETHRLEUVALIETHR 325
        |||
Db      985 CCCATCTCTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1044
OY      326 SERMETSERARGYLSLEUVALIETHRLEUVALIETHRLEUVALIETHRLEUVALI 345
        |||
Db      1045 TCTGTGAGCAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1104
OY      346 SERVALSERTHRLEUVALIETHRLEUVALIETHRLEUVALIETHRLEUVALI 359
        |||
Db      1105 TCTGTTCACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1146

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KW      rheumatoid arthritis; inflammatory bowel disease;
KM      chronic lung inflammation; treatment; antibody;
KW      affinity purification; detection; ss.
XX      Homo sapiens.
XX      US5440021-A.
XX      08-AUG-1995.
XX      29-MAR-1991. 91US-0677211.
XX      25-FEB-1994. 94US-0202056.
XX      29-MAR-1991. 91US-0677211.
PA      (CHUN/) CHUNTHARAPAI A.
PA      (HEBE/) HEBERT C.
PA      (KIMK/) KIM K J.
PA      (LEEJ/) LEE J.
XX      Chuntcharapai A, Hebert C, Kim KJ, Lee J;
XX      WPI; 1995-283151/37.
XX      DR      P-PSDB; AAR80757.
XX      PT      New antibodies against interleukin 8 type B receptor - used to treat
XX      PT      or prevent inflammation, also for detecting receptor expression and
XX      PS      purification.
XX      Example 2: Columns 47-50; 62pp; English.
XX      CC      Antibodies directed against the interleukin-8 receptor B can be used
XX      CC      to treat or prevent inflammation e.g. psoriasis, dermatitis,
XX      CC      rheumatoid arthritis and particularly inflammatory bowel disease and
XX      CC      chronic lung inflammation. When immobilised, these antibodies may
XX      CC      be used to detect interleukin-8 receptor B expression in cells and
XX      CC      tissues and for affinity purification of interleukin-8 receptor B
XX      CC      from cells. This sequence is an additional chemokine superfamily
XX      CC      receptor which was identified by probing lambda libraries of genomic
XX      CC      DNA from a human monocyte-like cell line (U-60) and human peripheral
XX      CC      blood lymphocytes using a large fragment of the interleukin-8 type
XX      CC      A receptor DNA (See AA099006).
XX      SQ      Sequence 1737 BP; 454 A; 411 C; 373 G; 499 T; 0 other;
SQ      Alignment Scores:
Pred. No.: 3.84e-187 Length: 1737
Score: 1678.50 Matches: 319
Percent Similarity: 95.48% Conservative: 19
Best Local Similarity: 90.11% Mismatches: 11
Query Match: 89.90% Indels: 5
DB: 16 Gaps: 1
US-09-367-052-2 (1-359) x AA099007 (1-1737)
OY      6  VALSERILETHRLEUARGSERMETTHRASPPLYSTYRARGHLSLEUSERVALA 25
        |||
Db      100 ATCATCTATATCACTTCACTGACATACACGAGAAATGGCTGACGACATGACTCC 159
OY      26  ASNLGSLUPLROCYSPHEARGSPGLUASVALHLSPHEASNAARGYIETHRLEUPROTH 45
        |||
Db      160 ATGAGGAAACCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 219
OY      46  ILETRYRHEIETHRLEUVALIETHRLEUVALIETHRLEUVALIETHRLEUVALIETH 65
        |||
Db      220 ATCTACTCATCATCTTCTTAACGTGGCAATGTGGCAATGGATGGTCACTCTGTCATG 279
OY      66  GATYTGILNLSYLSLEUARGSERMETTHRASPPLYSTYRARGHLSLEUSERVALA 85
        |||
Db      280 GGTACCAAGAACTGAGAACATGACGACGACAACTACAGGCTGCACTGTCAGTGCC 339
OY      86  ASPLLEUAPHEVALIETHRLEUPROPHETRPALAVASPALAMETALAASPTPTYR 105
        |||

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D 340 GACCTCCTTTTTCATCAGCGCTTCCTTCTGGGAGTTGATCCGTGGCAAACTGGTAC 399
Q 106 PheGlyLysPheLeuLysLysAlaValHisIleIleTyrThrValAsnLeuTyrSer 125
D 400 TTGGGAACTTCTTATGCAAGGAGTCCATGTCATCTACACATCACTTACAGCAGT 459
Q 126 ValLeuIleLeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaTyrAsn 145
D 460 GTCCATCCTCGCTTCATCAGTCTGGACCGCTACCTGGCCATCGTCCAGCCACACAC 519
Q 146 SerGlnArgProArgLysLeuLeuAlaGluLysAlaValTyrValGlyValTyrPhePro 165
D 520 AGTCAAGAGCCCAAGAGAGCTGTGGCTGAAAGAGTGTATGTTGGCTGTGGATCCCT 579
Q 166 AlaLeuLeuLeuThrIleProAspPheIlePheAlaAspValSerGlnGlyAspIleSer 185
D 580 GCCCTCTGCTGATTCCTCCGACTTCATCTTTGCCAACGTC-----AGT 624
Q 186 GlnGlyAspAspArgTyrIleCysAspArgLeuTyrProAspSerLeuTyrMetValVal 205
D 625 GAGCAGAGATGACAGATATATCTGTGACCGCTTACCCCAATGACTGTGGGTGTGG 684
Q 206 PheGlnPheGlnHisIleMetValGlyLeuIleLeuProGlyIleValIleLeuSerCys 225
D 685 TTCCAGTTTCAGCAGATCATGATGTTGGCTTATCTGCTGATTTGTTCATCTCTGCTGC 744
Q 226 TyrCysIleIleIleSerLysLeuSerHisSerLysGlyHisGlnLysArgLysAlaLeu 245
D 745 TATTGCATTATCATCTCCAAAGCTGTCACACTCCAAAGGCCACAGAGCCAGCCCTC 804
Q 246 LysThrThrValIleLeuIleLeuAlaPhePheAlaCysTyrPheProTyrTyrValGly 265
D 805 AAGACCAGATCATCTCTCATCTGCTGCTTCTGCTGCTGCTGCTGCTTACTCATTTGGG 864
Q 266 IleSerIleAspSerPheIleLeuLeuGlyValIleLysGlnGlyLysAspPheGlySer 285
D 865 ATCAGCATGACTCTTCATCTCTGAGCAATCATCAAGCAAGGAGTGAATTTGGAGAAC 924
Q 286 IleValHisLysTyrPheSerIleThrGlnAlaLeuAlaPhePheHisCysCysLeuAsn 305
D 925 ACTGTCCACAGATGATTCATCCATCCAGGCGCTTCTTCCACAGTGTGTCTGAGAC 984
Q 306 ProIleLeuTyrAlaPheLeuGlyAlaLysPheLysSerSerAlaGlnHisAlaLeuAsn 325
D 985 CCCATCTCTATGCTTCTCTGGAGCCAAATTTAAACCTCTGCCAGCAGCAGCATCCACC 1044
Q 326 SerMetSerArgLysSerSerLeuLysIleLeuSerLysGlyLysArgGlyGlyHisSer 345
D 1045 TCTGTAGCAGAGGTCACAGCTCAAGATCTCTCCAAAGGAAGGAGGAGTGAGCATTTCA 1104
Q 346 SerValSerThrGlnSerLysSerSerPheHisSerSer 359
D 1105 TCTGTTCCAGTGTGAGTGTCTTCAAGTTTTCATCTCCAGC 1146
RESULT 14
AB197982
ID AB197982 standard: cDNA; 1059 BP.
AC AB197982:
XX
XX 18-FEB-2002 (first entry)
XX
XX Non-endogenous human GPCR cDNA, SEQ ID NO: 484.
XX
XX Human: G protein-coupled receptor; GPCR; non-endogenous; mutant;
XX constitutively activated GPCR; agonist; disease; ss.
OS Homo sapiens.
OS Synthetic.
XX
XX MO200177172-A2.
XX
XX 18-OCT-2001.
PD
```

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XX
XX 05-APR-2001; 2001WO-US11098.
XX
XX 07-APR-2000; 2000US-195747P.
XX
XX (AREN-) ARENA PHARM INC.
XX
XX Lehmann-Brunnsma K, Liaw CW, Lin I;
XX
XX MPI: 2001-648759/74.
XX
XX P-PSDB; ABB56346.
XX
XX Identifying agonists of G protein-coupled receptors (GPCRs) for use in
XX disease treatment, comprises contacting candidate compounds with
XX versions of GPCRs -
XX
XX Example 2; Page 284-285; 394pp; English.
XX
XX The invention relates to G protein-coupled receptors (GPCRs) for which
XX the endogenous ligand has been identified. Non-endogenous
XX constitutively activated versions of known GPCRs are used in the
XX invention for the direct identification of candidate compounds as
XX receptor agonists, inverse agonists or partial agonists. Such
XX agonists are useful as therapeutic agents for diseases or disorders
XX associated with GPCRs. The present sequence encodes a non-endogenous
XX version of a known human GPCR.
XX
XX Sequence 1059 BP; 246 A; 299 C; 233 G; 281 T; 0 other;
```

Alignment Scores:

```
Pred. No.: 9,366-187 Length: 1059
Score: 1672.50 Matches: 318
Percent Similarity: 95.20% Conservative: 19
Best Local Similarity: 89.83% Mismatches: 12
Query Match: 23 Indels: 5
DB: Gaps: 1
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US-09-367-052-2 (1-359) x AB197982 (1-1059)

```
Q 6 ValSerIleTyrThrSerAspAsnTyrSerGlnGluValGlySerGlyAspTyrAspSer 25
D 10 ATCAGATATATACATTCATCAGATATACATCCAGGAAATGGCTCAGGGAGCATATACATCC 69
Q 26 AsnLysGluProCysPheArgAspLysAsnValHisPheAspArgIlePheLeuProThr 45
D 70 ATGAGGAGAACCTGTTTCCGTGAGAAATGCTAATTTCAATAAATGTCCTGCCACAC 129
Q 46 IleTyrPheIleIlePheLeuThrGlyIleValGlyAsnGlyLeuValIleLeuValMet 65
D 130 ATCTACTCCATCATCTTCTTAACTGGCAATTTGGGCAATGCAATGTCATCTGCTGATCATG 189
Q 66 GlyTyrGlnLysLysLeuArgSerMetThrAspLysTyrArgLeuHisLeuSerValAla 85
D 190 GGTTCACGAAAGAAATCTGAGAGCATGACGACAGATGACAGGCTCCACCTGTCAAGTGC 249
Q 86 AspLeuLeuPheValIleThrLeuProPheThrPalaValAspAlaMetAlaAspTyrPyr 105
D 250 GACCTCCTCTTGTGCATACGCTTCCCTTCTGGAGTTGATGCCGTGGCAACTGTGATC 309
Q 106 PheGlyLysPheLeuLysLysAlaValHisIleIleTyrThrValAsnLeuTyrSerSer 125
D 310 TTGGGAACTTCTTATGCAAGGAGTCCATGTCATCTACACATCACTTACAGCAGT 369
Q 126 ValLeuIleLeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaTyrAsn 145
D 370 GTCTCATCTCGCTTCATCAGTGTGGACCGCTCAAGCTGTGCCATGTCCAGCCACAC 429
Q 146 SerGlnArgProArgLysLeuLeuAlaGluLysAlaValTyrValGlyValTyrPhePro 165
D 430 ACTCAGAGGCCAAGAGACTGTGTGCTGAAAGAGTGTATGTTGGGTCTGATTCCT 489
Q 166 AlaLeuLeuLeuThrIleProAspPheIlePheAlaAspValSerGlnGlyAspIleSer 185
D
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Db 490 GCCCTCTGCTGACTATTCCGACATTCATTCTTTGCCAAGCTC-----AGT 534
Oy 186 GlnGlyAspAspArgTyrIleCysAspArgLeuTyrProAspSerLeuTrpMetVal 205
Db 535 GAGGAGATGACAGATATATCTGTGACCGCTTCCCAATCCCAAGACTTGGGTGGTGG 594
Oy 206 PheGlnPheGlnHisIleMetValGlyLeuIleLeuProGlyIleValIleLeuSerCys 225
Db 595 TTCGATTTTCAGACATCATGTTGGCTTATCCGCCGATATGTCTATCTGTCCGCGC 654
Oy 226 TyrCysIleIleIleSerLeuSerHisSerIleSerIleGlyHisGlyAspGlyAlaLeu 245
Db 655 TATTCATTATCATCTCCAAAGCTGTCCACACTCCAAAGGGCCACCAAGGCCAAGCCAG 714
Oy 246 LysTrpTrpValIleLeuIleLeuAlaPhePheAlaCysTrpLeuProTyrTyrValGly 265
Db 715 AAGACACAGTATCTCTATCTGCTGCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTG 774
Oy 266 IleSerIleAspSerPheIleLeuLeuGlyValIleIleGlyHisGlyAspPheGlySer 285
Db 775 ATCAGCATGAGCTCTTCTATCTCTCTCTGGAATCATCAAGCAAGGGGTGAGTTGAGAAC 834
Oy 286 IleValHisLysTrpIleSerIleThrGlyAlaLeuAlaPhePheHisCysCysLeuAsn 305
Db 835 ACTGTGCACAACTGATTTCCATCCAGCCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTG 894
Oy 306 ProIleLeuTyrAlaPheLeuGlyAlaLysPheLysSerSerAlaGlnHisAlaLeuAsn 325
Db 895 CCCATCTCTATGCTTCTTCTGAGCCCAATTTAAACCTCTGCCCAGACCCACTCACC 954
Oy 326 SerMetSerArgGlySerSerLeuLysIleLeuSerIleGlyLysArgGlyLysHisSer 345
Db 955 TCTGTGAGAGAGAGGAGCCAGCTCAAGATCTCTCCAAAGAAAGCAAGGAGTGACATTCA 1014
Oy 346 SerValSerThrGlySerGlyLeuSerSerSerPheHisSerSer 359
Db 1015 TCTGTTTCCACTGAGTGTGAGTCTTCAAGTTTCACTCACC 1056

RESULT 15
AAV18357
ID AAV18357 standard; DNA; 1317 BP.
XX
AC AAV18357;
XX
DT 25-SEP-1998 (first entry)
XX
DE Human RM3 seven transmembrane (7TM) receptor cDNA.
V28: placenta; seven transmembrane receptor; 7TM; signal transduction;
immunology; inflammation; RM3; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 201..1211
FT /tag= a
FT /product= "Human RM3 seven transmembrane receptor"
XX
PN US5759804-A.
XX
PD 02-JUN-1998.
XX
PF 17-NOV-1993; 93US-0153848.
XX
PR 17-NOV-1992; 92US-0977452.
XX
PA (ICOS-) ICOS CORP.
XX
PI Godiska R, Gray PW, Schweickart VL;
XX
DR WPI: 1998-332132/29.
XX
P-PSDB: AAV48734.
XX

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PT DNA encoding V28 seven transmembrane receptor polypeptide - useful
PT for producing recombinant polypeptide and anti-V28 antibodies, and
PT in screening assays for V28 agonists and antagonists
PS Example 11: Columns 89-94; 56pp; English.
XX
CC The present novel sequence represents the human RM3 cDNA isolated
CC from a human macrophage cDNA library. The invention claims for
CC the full length V28 genomic DNA sequence (AAV18343) isolated from a
CC human placenta genomic library. The V28 (AAW48722) and RM3 proteins are
CC seven transmembrane (7TM) receptors which are probably involved in
CC signal transduction. The invention also claims that cells transformed
CC with V28 DNA can be used to produce the recombinant polypeptide, to
CC produce anti-V28 antibodies or in screening assays for V28 agonists or
CC antagonists. The antibodies, agonists and antagonists could then be
CC used to modulate V28 receptor-ligand binding, for e.g. in Immunological
CC and/or inflammatory events in vivo.
XX
SQ Sequence 1317 BP; 332 A; 342 C; 265 G; 378 T; 0 other:
Alignment Scores:
Pred. No.: 1,29e-186 Length: 1317
Score: 1672.50 Matches: 318
Percent Similarity: 95.20% Conservative: 19
Best Local Similarity: 89.83% Mismatches: 12
Query Match: 89.58% Indels: 5
DB: 19 Gaps: 1
US-09-367-052-2 (1-359) x AAV18357 (1-1317)
Oy 6 ValSerIleTyrThrSerAspAsnTyrSerGlnGlyValGlySerGlyAspTyrAspSer 25
Db 165 TTGCAATATATACACTTCAAGATACATACACGAGAAATGGGTGAGGAGACTATACATCC 224
Oy 26 AsnLysGluProCysPheArgAspGlnAsnValHisPheAsnArgIlePheLeuProThr 45
Db 225 ATGAAGGAACCTGTTCCGTGGAAGAAATGCTAATTAATTAATCTTCCGCTCCACCC 284
Oy 46 IleTyrPheIleIlePheLeuThrGlyIleValGlyAsnGlyLeuValIleLeuValMet 65
Db 285 ATCTACTCCATCATCTTCTTAACGTGAGTGGGCAATGATGTGCTATCTGCTGCTATG 344
Oy 66 GlyTyrGlnLysLysLeuArgSerMetThrAspLysTyrArgLeuHisLeuSerValAla 85
Db 345 GGTTCACAGAGAACTGAGAAAGCATGACGAGCAAGTACAGCTCAGCTGACATGGCC 404
Oy 86 AspLeuLeuPheValIleThrLeuProPheTrpAlaValAspAlaMetAlaAspTrpTyr 105
Db 405 GACCTCTCTTGTGCATACAGCTTCCCTTGTGGCAGTTGATGCGCGCAACCTGGTAC 464
Oy 106 PheGlyLysPheLeuCysLysAlaValHisIleIleTyrThrValAsnLeuTyrSerSer 125
Db 465 TTTGGGAACCTCTATGCAAGGAGGAGTGCATCATCAACAGTCAACCTCTACAGCAGT 524
Oy 126 ValLeuIleLeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThrAsn 145
Db 525 GTTCATCTCTGCTTCTTATCATGCTGAGACCGCTACCTGCGCATGCTCAGCCACAC 584
Oy 146 SerGlnArgProArgLysLeuLeuAlaGlyLysAlaValTyrValGlyValTrpIlePro 165
Db 585 AGTCAGAGGCCAAGAGAGCTGTTGGCTGAAAAGGGTGTATGTTGGGCTCGATCCCT 644
Oy 166 AlaLeuLeuLeuThrIleProAspPheIlePheAlaAspValSerGlnGlyAspIleSer 185
Db 645 GCCCTCTGCTGACTATTCGCCGACTTCCTTCCCAACGTC-----AGT 689
Oy 186 GlnGlyAspAspArgTyrIleCysAspArgLeuTyrProAspSerLeuTrpMetValVal 205
Db 690 GAGGAGATGACAGATATATCTGTGACCGCTTCTTCCCAATGACTTGGGTGGTGTGTG 749
Oy 206 PheGlnPheGlnHisIleMetValGlyLeuIleLeuProGlyIleValIleLeuSerCys 225
Db 750 TTCAGATTTCACACATCATGTTGGCTTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 809

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QY 226 TyrCysIleIleIleSerLysLeuSerHisSerLysGlyHisGlnLysArgLysAlaLeu 245
 DB 810 TATTCATTATCATCTCCAGCTGCACACTCCAGGCCACCAAGCCGACGCCCTC 869
 QY 246 LysThrThrValIleLeuIleLeuAlaPhePheAlaCysTrpLeuProTyrTyrValGly 265
 DB 870 AAGACCACAGTCATCTCATCTCTGCTTCTGCGCTGTGCGCTTACTACATGCG 929
 QY 266 IleSerIleAspSerPheIleLeuLeuGlyValIleLysGlnGlyCysAspPheGlnSer 285
 DB 930 ATCAGCATCGACTCTTCTATCTCTCTGGAATCATCAAGCAAGGTGTGAGTTGAGAAC 989
 QY 286 IleValHisLysTrpIleSerIleThrGlnAlaLeuAlaPhePheHisCysCysLeuAsn 305
 DB 990 ACTGTGCACAGAGTGATTTCCATCCACGAGGCCCTAGCTTCTCTTCCACTGTGTGTAAC 1049
 QY 306 ProIleLeuTyrAlaPheLeuGlyAlaLysPheLysSerSerAlaGlnHisAlaLeuAsn 325
 DB 1050 CCCATCTCTATGCTTCTTCTGAGCCAAATTTAAACCTCTGCCACGACGCACTCAC 1109
 QY 326 SerMetSerArgGlySerSerLeuLysIleLeuSerLysGlyLysArgGlyGlyHisSer 345
 DB 1110 TCTGTGACGACAGGGGTCCAGCTCCAGATCCTCTCCAAAGGAAAGCGAGGTGGACATTCA 1169
 QY 346 SerValSerThrGlnSerGlnSerSerSerPheHisSerSer 359
 DB 1170 TCTGTTCACAGACTGAGTGTCAAGTTTTCACCTCCAGC 1211

Search completed: July 12, 2003, 17:14:34
 Job time : 222 secs

Db	86	TTCAAGTATATACACTTCAGATAACTACACCGAGAAATGGGCTGACGGGACTATGATCC	145
OY	26	ASnlYsgIuPrOCysPheIatrgAsPcIuAsnValHisPheAsnArgIlePheLeuProthr	45
Db	146	ATGAGGAACCCCTGTTCCTCGGAAGAAATCCTAATTTCAATAAATTTCTCTCGCCACC	205
OY	46	IleIyrrPheIleIlePheLeuThrGlyIleValGlyAsnGlyLeuValIleLeuValMet	65
Db	206	ATCTACTCCATCATCTTCTTAACTGGCATTTGTGGCAATGGATTTGGTATCTGGTCTATG	265
OY	66	GIyTyrGIuLysLysLeuArgSerMetThrAspLysTyrArgLeuHisLeuSerValAla	85
Db	266	GGTTACCGAGAAACGTGAGAACGATGACGACAAAGTACAGGCTCCACCTGCACTGGCC	325
OY	86	AspLeuLeuPheValIleThrLeuProPheThrAlaValAspAlaMetAlaAspIrrYr	105
Db	326	GACCTCCTCTTTGTATCATCCGCTTCCTCTTGCGGAGTTGATGGCTGGCAACATGGTAC	385
OY	106	PheGIyLysPheLeuCysLysAlaValHisIleIleYrrThrValAsnLeuTyrSerSer	125
Db	386	TTTGGGAACCTCTATGCAAGCAGTCCATGTCATCTACACGTCACACTGATCAGCAGT	445
OY	126	ValLeuIleLeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThrAsn	145
Db	446	GTCTCATCCCGGCTTCATCAGTCTGACCGCATCCGGCATCTGTCACGCCACAC	505
OY	146	SerGlnArgProArgLysLeuLeuAlaGluLysAlaValTyrValGlyValThrIlePro	165
Db	506	AGTAGAGAGCCACAGAAAGCTGTGGCTGTAAAGGGTCTATTTGGGCTGTGATCCCT	565
OY	166	AlaLeuLeuLeuThrIleProAspPheIlePheAlaAspValSerGlnGlyAspIleSer	185
Db	566	GCCCTCCGCGAGATATCCCGACTTCATCTTGGCAACGTC-----AGT	610
OY	186	GlnGlyAspAspArgTyrIleCysAspArgLeuTyrProAspSerLeuTrpMetValVal	205
Db	611	GAGGCAGATGACAAATATATGTGTGACCGCTTACCCCAATGACTTGTGGGTGGTTGTG	670
OY	206	PheGlnPheGlnHisIleMetValGlyLeuIleLeuProGlyIleValIleLeuSerCys	225
Db	671	TTCCAGTTTCAGCACAATCATGATGGTGGCTTATTCGCTGGATTTGTGATCTGTGCTGC	730
OY	226	TyrCysIleIleIleSerLysLeuSerHisSerLysGlnHisGlnLysArgLysAlaLeu	245
Db	731	TATTCGATTTACATCTCCAAAGCTGTACACATCCAAAGGCCACACGAAAGGCCACCTC	790
OY	246	LysThrThrValIleLeuIleLeuAlaPhePheAlaCysTrpLeuProTyrTyrValGly	265
Db	791	AAGACACAGCATCTCATCTGTGGCTTTTTCGCCCTGTGGCTGTCCCTTAACTACTGTGG	850
OY	266	IleSerIleAspSerPheIleLeuLeuGlyValIleLysGlnGlyCysAspPheLeuSer	285
Db	851	ATTCAGCATCGACCTTCATCTCCTCGGAATTCATCAAGGAGGTGTGAGATTGAGAAC	910
OY	286	IleValHisLysTrpIleSerIleIleThrGlnAlaLeuAlaPhePheHisCysCysIleuAsn	305
Db	911	ACTGTGACAAAGTGGATTTCCATACCGGAGGCCCTAGGCTTTCCTCCACTGTGTGTGAC	970
OY	306	ProIleLeuTyrAlaPheLeuGlyAlaLysPheLysSerSerAlaGlnHisAlaLeuAsn	325
Db	971	CCCATCTCTATAGCTTTCTTGGAGCCAAATTTAAACCTGTGCCACAGCAGCTACAC	1030
OY	326	SerMetSerArgLysSerSerLeuLysIleLeuSerLysGlyLysArgGlyGlyHisSer	345
Db	1031	TCTGTGAGAGAGGGCTCAGGCTCAAGATCTCTTCCAAAGGAAAGCGAGTGGACATTC	1090
OY	346	SerValSerThrGluSerGluSerSerSerPheHisSerSer	359
Db	1091	TCGTGTTCACATGAGCTGAGTCTTCAAGTTTCACTTCACAC	1132

```

? Patent No. 6391567
?
? GENERAL INFORMATION:
?
? APPLICANT: Lifteman, Dan R.
?
? APPLICANT: Kwon, Douglas S.
?
? APPLICANT: van Kooyk, Yvette
?
? APPLICANT: Geljtenbeck, Theo
?
? TITLE OF INVENTION: METHODS OF USING A FACILITATOR OF RETROVIRAL ENTRY INTO
?
? TITLE OF INVENTION: CELLS
?
? FILE REFERENCE: 1049-1-017
?
? CURRENT APPLICATION NUMBER: US/09/517,605
?
? CURRENT FILING DATE: 2000-03-02
?
? NUMBER OF SEQ. ID NOS.: 17
?
? SOFTWARE: PatentIn Ver. 2.0
?
? SEQ. ID NO. 14
?
? LENGTH: 1679
?
? TYPE: DNA
?
? ORGANISM: Homo sapiens
?
? OS-09-517-605-14

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Alignment Scores:		
Prod. No.:	3, 13e-188	length: 1679
Score:	1678.50	Matches: 319
Percent Similarity:	95.488	Conservative: 11
Best Local Similarity:	90.118	Mismatches: 19
Query Match:	89.908	Indels: 5
DB:	4	Gaps: 1

QY	6	ValSerIleTyrThrSerAspAsnTyrSerGluGluValaGlySerGlyAspTyrAspSer	25
Db	98	ATCAGATATATACACTTCACATACACACCGAAGAAATGGGCTCAGGGGACTAGACTCC	157
QY	26	AsnLysGluProCysPheArgAspGlnAsnValHisPheAsnArgIlePheLeuProThr	45
Db	158	ATGAGAGAACCCGTGTTCCGTGCAAGAAATGCTAATTTCATTAATAACTTCCTGCCACC	217
QY	46	IleTyrPheIleIlePheLeuThrCylIleValaGlyAsnGlyLeuValIleIleValMet	65
Db	218	ATCTACTCATCATCTCTTAACTGCGACATGTGGGCAATGGATTTGGTCACTCCGTATG	277
QY	66	GlyTyrGlnLysLysLeuArgSerMetThrAspLysTyrArgLeuHisLeuSerVala	85
Db	278	GGTTACACAGAAACTGGAAGCATGACGGACAAGTACAGCGTCGACCTGTAGTGGCC	337
QY	86	AspLeuLeuPheValIleIleThrLeuProPheTrpAlaValaAspAlaMetAlaSerTrpTyr	105
Db	338	GACCTCTCTTGTGTCATCAGCGCTCTTCCTGGGAGTGTGTCGGCGGCAACTGGCTAC	397
QY	106	PheGlyLysPheLeuCysLysAlaValaHisIleIleTyrTrpValaAsnLeuTyrSerSer	125
Db	398	TTTGGGAACCTCTTATGCCAAGGCAGTCCATGTGCATCTACACAGTCAACCTCTACAGCAGT	457
QY	126	ValLeuIleLeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValaHisAlaTrpAsn	145
Db	458	GTTCCTATCTGGCTTCATCAGTCTGGACGGCTACCTGGCACTGCTCCACGCCACCAAC	517
QY	146	SerGlnArgProArgLysLeuLeuAlaLeuLysAlaValaTyrValaGlyValTrpIlePro	165
Db	518	AGTCAGAGGCCAAGGAACCTGTGGCTGTAAGAAAGGTGCTTATGTGGCGTCTGGATCCCT	577
QY	166	AlaLeuLeuLeuThrIleProAspPheIlePheAlaAspValSerGlnGlyAspIleSer	185
Db	578	GGCCCTCTGCTACATATTCGCCGACTTCATCTTTGGCAACGTC-----AGT	622
QY	186	GlnGlyAspAspArgTyrIleCysAspArgLeuTyrProAspSerLeuTrpMetVala	205
Db	623	GAGGCGATGACAGATATATCTGTGACCGCTTCTACACCCAAATGACTCTGTGGGTGGTGTG	682
QY	206	PheGlnPheGlnHisIleMetValaGlyLeuLeuLeuProGlyIleValIleLeuSerCys	225
Db	683	TTCCAGATTTCACACATCATGTTGGGCTTATCTCGCTGGTATTTGTCATCCGTGCTCG	742

Db 985 CCCATCTCTATGCTTCTCTTGAGCCAAATTTAAACCTCTGCCACGACCTCACC 1044
QY 326 SerMetSerArgGlySerSerLeuLysIleLeuSerLysGlyLysArgGlyLysSer 345
Db 1045 TCTGTGAGCAGAGGGGTCCAGCTCAGATCCTCTCCAAAGAAAGCGAGGTGACATTCA 1104
QY 346 SerValSerThrGluSerGluSerSerSerPheHisSerSer 359
Db 1105 TCTGTTCCACTGAGTCTGAGTCTTCAAGTTTTCACCTCAGC 1146

RESULT 4

US-08-076-093A-3
Sequence 3, Application US/08076093A
Patent No. 5543503

GENERAL INFORMATION:

APPLICANT: Chuncharapal, Anan
APPLICANT: Lee, James
APPLICANT: Hebert, Caroline
APPLICANT: Jin Kim, K.
TITLE OF INVENTION: Antibodies to Human PFAA Receptors
NUMBER OF SEQUENCE ADDRESSES: 6
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 Inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/076,093A
FILING DATE: 11-Jun-1993
CLASSIFICATION: 530
PRIOR APPLICATION NUMBER: 07/810782
FILING DATE: 19-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/677211
FILING DATE: 29-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 706P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1737 nucleotides
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear

US-08-076-093A-3

Alignment Scores:

Pred. No.: 3,296-188 Length: 1737
Score: 1678.50 Matches: 319
Percent Similarity: 95.48% Conservative: 19
Best Local Similarity: 90.11% Mismatches: 11
Query Match: 89.90% Indels: 5
DB: 1 Gaps: 1

US-09-367-052-2 (1-359) x US-08-076-093A-3 (1-1737)

QY 6 ValSerIleThrValThrSerAspAspArgSerGluGluValGlySerGlyAspTyrAspSer 25
Db 100 ATCAGTATATACACTTTCAGATACACCGAGAAATGGCTCAGGGGACTATGACTCC 159

QY 26 AsnLysGluProCysPheArgAspGluAsnValHisPheAsnArgIlePheLeuProThr 45
Db 160 ATGAAGAGAACCTGTTTCCGGAGAAATGCTAATTTCATTAATCTCTCCACC 219
QY 46 IleThrPheIleIlePheLeuThrGlyIleValGlyAsnGlyLeuValIleLeuValMet 65
Db 220 ATCTACCTCCATCATTCTTAACTGGCATTTGGGCAATGATTTGATCTCTGTCATG 279
QY 66 GlyThrGlnLysLysLeuArgSerMetThrAspLysTyrArgLeuHisLeuSerValAla 85
Db 280 GGTTCACAGAAAGAACTGAGAGCATGACGAGCAAGATGACGGCTGCACCTGTCACTG 339
QY 86 AspleuLeuPheValIleThrLeuProPheThrPalaValAspAlaMetAlaAspTyr 105
Db 340 GACCTCCCTTTGTCATCAGCCTTCCCTTGGGAGATGATGGCGTGGCAACTGGTAC 399
QY 106 PheGlyLysPheLeuCysLysAlaValHisIleIleThrValAsnLeuTyrSerSer 125
Db 400 TTGGGAACTTCCATGCAAGGAGTCATCTCATACAGTCACCTTCACAGCAGT 459
QY 126 ValLeuIleLeuAlaPheIleSerLeuAspArgTyrIleValIleValHisAlaThrAsn 145
Db 460 GTCCCTATCTGGCCTTATCAGTGTGACCGCTACCTGGCATCTGCACGCCACCAAC 519
QY 146 SerGlnArgProArgLysLeuLeuAlaGluLysAlaValTyrValGlyValTyrPhePro 165
Db 520 AGTCAGAGCCAGAGAACTGTGGCTGAAGAAGTGTATGTGGGTGTGATCCCT 579
QY 166 AlaLeuLeuLeuThrIleProAspPheIlePheAlaAspValSerGlnGlyAspIleSer 185
Db 580 GCCCTCCGCTGACTATCCCGACTTCTTCCCAACGTC-----AGT 624
QY 186 GlnGlyAspAspArgTyrIleCysAspArgLeuTyrProAspSerLeuTyrPheValVal 205
Db 625 GAGCAGATGACAGATATATCTGTGACCGCTTCTACCCCAATGACTGTGGTGTGTG 684
QY 206 PheGlnPheGlnHisIleMetValGlyLeuIleLeuProGlyIleValIleLeuSerCys 225
Db 685 TTCCAGTTTCAGCAGATCATGTGGCTTATCTGCTGATTTGATTCATCTGCTGTC 744
QY 226 TyrCysIleIleIleSerLysLeuSerHisSerLysGlyHisGlnLysArgLysAlaLeu 245
Db 745 TATTGCATTATCATCTCCAAAGCTGTCCACATCCAAAGGCCACAGAACCCGACCCCTC 804
QY 246 LysThrThrValIleLeuIleLeuAlaPhePheAlaCysTyrLeuProTyrValGly 265
Db 805 AAGACACAGATCATCTATCTGTGCTTCTTGGCTGTGGCTGTACTTACTATTTGGG 864
QY 266 IleSerIleAspSerPheIleLeuLeuGlyValIleLysGlnGlyCysAspPheGluSer 285
Db 865 ATCAGCATCGACTCCTTCATCTCCTCGGAATTCATCAAGAGGTGTGACTTTGAGAAC 924
QY 286 IleValHisLysTyrPheIleSerIleThrGluAlaLeuAlaPhePheHisCysCysLeuAsn 305
Db 925 ACTGTGCACAAAGTGAATTCATCACCGAGGCCCTTACCTTCTTCACATGTTGCTGAC 984
QY 306 ProIleLeuTyrAlaPheLeuGlyAlaLysPheLysSerSerAlaGlnHisAlaLeuAsn 325
Db 985 CCCATCTCTATGCTTCTTCTGGAGCCAAATTTAAACCTTGGCCACGACCTCACC 1044
QY 326 SerMetSerArgGlySerSerLeuLysIleLeuSerLysGlyLysArgGlyLysSer 345
Db 1045 TCTGTGAGCAGAGGGGTCCAGCTCAGATCCTCTCCAAAGAAAGCGAGGTGACATTCA 1104
QY 346 SerValSerThrGluSerGluSerSerSerPheHisSerSer 359
Db 1105 TCTGTTCCACTGAGTCTGAGTCTTCAAGTTTTCACCTCAGC 1146

RESULT 5

US-08-701-265-3

Sequence 3, Application US/0801265
Patent No. 5776457
GENERAL INFORMATION:

APPLICANT: Chuntharapai, Anan
APPLICANT: Lee, James
APPLICANT: Hebert, Caroline
APPLICANT: Jin Kim, K.
TITLE OF INVENTION: Antibodies to Human PFA Receptors
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/701,265
FILING DATE: 22-AUG-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/076093
FILING DATE: 11-Jun-1993
APPLICATION NUMBER: 07/810782
FILING DATE: 19-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/677211
FILING DATE: 29-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 706P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1737 nucleotides
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
US-08-701-265-3
Alignment Scores:
Seq. No.: 3,29e-188 Length: 1737
Identical Similarity: 1678.50 Matches: 319
Best Local Similarity: 95.48% Conservative: 19
Query Match: 89.90% Mismatches: 11
Indels: 5
Gaps: 1
US-09-367-052-2 (1-359) x US-08-701-265-3 (1-1737)
QY 6 ValSerIleYrThrSerAspAsnTyrSerGluGluValGlySerGlyAspTyrAspSer 25
DB 100 ATCAGTATATACCTTCAGATACACCGAGAAATGGGCTCAGGGAGCTATGACTCC 159
QY 26 AsnLysGluProCysPheArgAspGluAsnValHisPheAsnArgIlePheLeuProThr 45
DB 160 ATGAAGAAACCCGTTCCGTGGAAGAAATGCTATTCATTAATAATCTCTCCGCCACC 219
QY 46 IleYrPheIleIlePheLeuThrGlyIleValGlyAsnGlyLeuValIleLeuValMet 65
DB 220 ATCTACTCCATCCTCTTCTTACTGCGCATTCGTGGCATGATGGTCATCTGCTCATG 279
QY 66 GlyTyrGlnLysLysLeuArgSerMetThrAspLysTyrArgLeuHisLeuSerValAla 85
DB 280 GGTTCAGCAAGAAAGCTGAGAAAGCTGACGCAAGAGTACAGAGGCTCAGCTGCTGAGCC 339
QY 86 AspleuLeuPheValIleThrLeuProPheThrAlaValAspAlaMetAlaAspTrpTyr 105

DB 340 GACCTCTCTTGCATCAGCCTTCCCTTGGGAGATTGACCGCTGCAACAGCTGAC 399
QY 106 PheGlyLysPheLeuCysLysAlaValHisIleIleYrThrValAsnLeuTyrSerSer 125
DB 400 TTTGGAACTTCATATGCAAGGAGCTCATCTCATACAGTCACAGTCAACCTTACAGCGT 459
QY 126 ValLeuIleLeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThrAsn 145
DB 460 GTCCCATCTGCGCTTATCATGCTGACCGCTACCTGCGCATCTGACGCCACAC 519
QY 146 SerGlnArgProArgLysLeuLeuAlaGlyLysAlaValTyrValGlyValTrpIlePro 165
DB 520 AGTCAGAGCCAGAAAGCTGTGGCTGAAGAAGGTCATGATGTTGGGCTGTGATCCCT 579
QY 166 AlaLeuLeuLeuThrIleProAspPheIlePheAlaAspValSerGlnGlyAspIleSer 185
DB 580 GCCCTCTGCTGACTATCCGACTTCATCTTGGCAACGTC-----AGT 624
QY 186 GlnGlyAspAspArgTyrIleCysAspArgLeuTyrProAspSerLeuTrpMetValAl 205
DB 625 GAGGAGATGACAGATATATCTGTGACCGCTTCTACCCCAATGACTGTGGGTGTG 684
QY 206 PheGlnPheGlnHisIleMetValGlyLeuIleLeuProGlyIleValIleLeuSerCys 225
DB 685 TTCAGATTTCAGACATCATGTGGCTTATCCGCTGATATTCATCTGCTGCTGCTG 744
QY 226 TyrCysIleIleIleSerLysLeuSerHisSerLysGlyHisGlnLysArgLysAlaLeu 245
DB 745 TATTGCATTATCATCTCCACCTGTCACATCCCAAGGCGCCACGAAAGCGGACCTTC 804
QY 246 LysThrThrValIleLeuIleLeuAlaPhePheAlaCysTrpLeuProTyrValGly 265
DB 805 AAGACACAGATCATCTATCTGCTTCTTCCCTTGGCTTGGCTGCTTACTACTGAG 864
QY 266 IleSerIleAspSerPheIleLeuLeuGlyValIleLysGlnGlyCysAspPheGluSer 285
DB 865 ATCAGCATGCACTCTTCATCTCTCTGGAATCATCAAGCAAGGCTGAGCTTGGAGAC 924
QY 286 IleValHisLysTrpIleSerIleThrGluAlaLeuAlaPhePheHisCysCysLeuAsn 305
DB 925 ACTGTGCACAGATGATTCATCACCGAGCCCTTCTTCTTCTTCTTCTTCTGAGAC 984
QY 306 ProIleLeuTyrAlaPheLeuGlyValAlaLysPheLysSerSerAlaGlnHisAlaLeuAsn 325
DB 985 CCCATCTCTATGCTTCTTCTGAGCCAAATTTAAACCTCTGCCCCACAGCAGCTCAC 1044
QY 326 SerMetSerArgGlySerSerLeuLysIleLeuSerLysGlyLysArgGlyHisSer 345
DB 1045 TCTGTGACACAGGGGTCCAGGCTCAAGATCTCTCCCAAGAAAGCAAGGAGGATTC 1104
QY 346 SerValSerThrGluSerGluSerSerPheHisSerSer 359
DB 1105 TCTGTTCACCTGAGTGTGAGTCTTCAAGTTTTCATCTCCAGC 1146
RESULT 6
US-08-284-586-3
Sequence 3, Application US/08284586
Patent No. 5840856
GENERAL INFORMATION:
APPLICANT: Chuntharapai, Anan
APPLICANT: Lee, James
APPLICANT: Hebert, Caroline
APPLICANT: Jin Kim, K.
TITLE OF INVENTION: Antibodies to Human PFA Receptors
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/284,586
FILING DATE:
CLASSIFICATION: 424
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/08/076,093A
FILING DATE: 11-Jun-1993
APPLICATION NUMBER: 07/810782
FILING DATE: 19-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/677211
FILING DATE: 29-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 706P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1737 nucleotides
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
US-08-284-586-3

Alignment Scores:

Pred. No.:	3,29e-188	Length:	1737
Score:	1678.50	Matches:	319
Percent Similarity:	95.48%	Conservative:	19
Best Local Similarity:	90.11%	Mismatches:	11
Query Match:	89.90%	Indels:	5
DB:	2	Gaps:	1

US-09-367-052-2 (1-359) x US-08-284-586-3 (1-1737)

QY 6 ValSerIleYrThrSerAspAsnTyrsSerGluGluValGlySerGlyAspTyAspSer 25
Db 100 ATCAGTATATACCTTCGATGACTAGACCCAGGAAATGGGCTCAGGGGACTATGACCTCC 159
26 AsnIysGluProCysPheArgAspGluAsnValHisPheAsnArgIlePheLeuProThr 45
Db 160 ATGAGAGAACCTCTTCCGCGAGAAATGCTAATTCATAAATCTTCTCCGCCACCC 219
46 IleYrPheIleIlePheLeuThrGlyIleValGlyAsnGlyLeuValIleLeuValMet 65
Db 220 ATCTACTCCATCATCTTCTTACTGCGATTGTGGCAATGGATGGTCATCTGCTCATG 279
66 GlyTyrglnIysLysLeuArgSerMetThrAspIlyTyArgLeuHisLysLeuSerValAla 85
Db 280 GGTACCAAGAAAGTGAAGAGCATGACGCAAGTACAGGCTGACCTGCTGAGTGGCC 339
86 AspleuLeuPheValIleThrLeuProPheThrAlaValAspAlaMetAlaAspTrpTyr 105
Db 340 GACCTCTCTTGTGATCAGCCCTTCCCTTGTGGCAGTGTATGCGGCAACTGGTAC 399
106 PheGlnPheGlnPheLeuCysLysAlaValHisIleIleYrThrValAsnLeuTySerSer 125
Db 400 TTTGGGAACCTTCATATGCAAGGAGTCCATGCTCATACAGCAACCTCTACAGCAGT 459
126 ValLeuIleLeuAlaPheIleSerLeuAspArgTyrglyLeuAlaIleValHisAlaThrAsn 145
Db 460 GTCTCATCTCGGCTTCATAGTCTGACCGCTACCTGCGGCATCTGACCGCCACCAAC 519
QY 146 SerGlnArgProArgLysLeuLeuAlaGluLysAlaValTyArgValTrpIlePro 165

Db 520 AGTCAGAGCCCAAGAGCTGTGGTGAAGAGGTGGTGTATGTGGCGTCTGCATCCCT 579
QY 166 AlaLeuLeuLeuThrIleProAspPheIlePheHisAlaSpValSerGlnGlyAspIleSer 185
Db 580 GCCCTCTGCTGACTATTCGCCGACTTATCTTGGCCACGC-----AGT 624
QY 186 GlnIysAspAspArgTyrlleCysAspArgLeuTyProAspSerLeuTrpMetValVal 205
Db 625 GAGCAGATGACAGATATATCTGTGACCCGCTTACCCCAATGACTGTGGGTGCTGTG 684
QY 206 PheGlnPheGlnHisIleMetValGlyLeuIleLeuProGlyIleValIleLeuSerCys 225
Db 685 TTCAGATTTCAGCAGCATGATGGTGGCTTATCCTGCTGGTATTCATCTCTGCTCC 744
QY 226 TyrcysIleIleIleSerLysLeuSerHisSerLysGlnHisGlnLysArgLysAlaLeu 245
Db 745 TATTGATATATCATCTCCAGAGCTGTCACTCCAGAGGCCACGAGAGCGAAGGCCCTC 804
QY 246 LysThrThrValIleLeuAlaPhePheAlaCysTrpLeuProTyTrpValGly 265
Db 805 AAGACACAGATCATCTCATCTGCTGCTTCCCTGCTGCTGCTGCTTACTACTGCG 864
QY 266 IleSerIleAspSerPheIleLeuLeuGlyValIleLysGlnGlyCysAspPheGlnSer 285
Db 865 ATCAGCATGCACTCTTCATCTCTCTGGAATCATCAAGAGGCTGTGAGATTGAGAAC 924
QY 286 IleValHisLysTrpIleSerIleThrGluAlaLeuAlaPhePheHisCysCysLeuAsn 305
Db 925 ACTGTGACAGATGATTCATCTGATCAGGAGCCCTTACTCTTCTGCTGCTGCTGCTG 984
QY 306 ProIleLeuTyAlaPheLeuGlyAlaLysPheLysSerSerAlaGlnHisAlaLeuAsn 325
Db 985 CCCATCCCTATGCTTCTTCTTGGAGCAATTAATTAACCTCTGCCAGCAGCAGCTCACC 1044
QY 326 SerMetSerArgLysSerLeuLysIleLeuSerLysGlyAsnArgGlyHisSer 345
Db 1045 TCTGTGAGCAGAGGCTCAGCTCAGATCTCTCCAAAGAGGAGGTGAGCATTTCA 1104
QY 346 SerValSerThrGlnSerGlnSerSerPheHisSerSer 359
Db 1105 TCTGTTCCAGCTGAGTCTGAGTCTTCAAGTTTCTACCTCCAGC 1146

RESULT 7
US-08-805-478-3
Sequence 3, Application US/08805478
Patent No. 5874543
GENERAL INFORMATION:
APPLICANT: Chuntharapal, Anan
APPLICANT: Lee, James
APPLICANT: Hebert, Caroline
APPLICANT: Jin Kim, K.
TITLE OF INVENTION: ANTIBODIES TO PFAA RECEPTOR
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/805,478
FILING DATE: 25-Feb-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/284586
FILING DATE: 10-AUG-1994
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/076093
FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/810782
FILING DATE: 19-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P0706P2P1C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1737 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
8-805-478-3

Alignment Scores:
Pred. No.: 3.29e-188 Length: 1737
Score: 1678.50 Matches: 319
Percent Similarity: 95.48% Conservative: 11
Best Local Similarity: 90.11% Mismatches: 19
Query Match: 89.90% Indels: 5
DB: 2 Gaps: 1

US-09-367-052-2 (1-359) x US-08-805-478-3 (1-1737)

QY 6 ValSerIleTyrThrSerAspAsnTyrSerGluGluValGlySerGlyAspTyrAspSer 25
Db 100 ATCAGTATATACCTTTCAGTATACACCGAGAAATGGCTCAGGGGACTATGACTCC 159

QY 26 AsnLysGluProCysPheArgAspGluAsnValHisPheAsnArgIlePheLeuProThr 45
Db 160 ATGAGGAAACCTCTTCCGTGAGAAATGCTATATTCAATAAATCTCTGCCACC 219

QY 46 IleTyrPheIleIlePheLeuThrGlyTLeValGlySngIleuValIleLeuValMet 65
Db 220 ATCTACTCCATCATCTTCTTACTGTCATGTCGTCATGTCGTCATGTCATGTCATG 279

QY 66 GlyTyrGlnLysLysLeuArgSerMetThrAspLysTyrArgLeuHisLeuSerValAla 85
Db 280 GGTACCAAGAAACAGCAAGACATGACGCAAGTACAGGCTGACCTGCTGCTGCC 339

QY 86 AspLeuLeuPheValIleThrLeuProPheTyrPalaValAspAlaMetAlaAspTyr 105
Db 340 GACCTCTCTTGTGATCAGCCTTCCCTTGGGCGAGTTGCGGCAACTGCTGAC 399

QY 106 PheGlyLysPheLeuCysLysAlaValHisIleIleTyrThrValAsnLeuTyrSerSer 125
Db 400 TTGTGGAACTTCATGCAAGGAGCTCCATGTCATACAGTCAACCTCTACAGAGT 459

QY 126 ValLeuIleLeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThrAsn 145
Db 460 GTCTCATTCCTGGCTTCATGCTGACCGCTACCTGCGCATCGTCCAGCCACCAAC 519

QY 146 SerGlnArgProArgLysLeuLeuAlaGlyLysAlaValTyrValGlyValTyrIlePro 165
Db 520 AGTCAGAGGCCCAAGAGAGCTGTCGTAAGAGCTGCTATGTTGGGCTGATCCCT 579

QY 166 AlaLeuLeuLeuThrIleProAspPheIlePheAlaAspValSerGlnGlyAspIleSer 185
Db 580 GCCCTCTGCTGACTATTCCTGCGCTTATCTTTCACACGCTC-----AGT 624

QY 186 GlnGlyAspAspArgTyrIleCysAspArgLeuTyrProAspSerLeuTyrMetValVal 205
Db 625 GAGGCAATGACATATATCTGACCGCTTACCCCATGACTTGTGGTGTGCTG 684

QY 206 PheGlnPheGlnHisIleMetValGlyLeuLeuLeuProGlyIleValIleLeuSerCys 225

Db 685 TTCAGTTTCAGACATCATGCTTGGCTTATCTCGCTGGTATGTATCATCTGCTGC 744

QY 226 TyrCysIleIleIleSerLysLeuSerHisSerLysGlyHisGlnLysArgLysAlaLeu 245

Db 745 TATTCATATATCATCTCCAAAGCTGTCACACTCCCAAGGCCACGAGAGCCAGGCCCTC 804

QY 246 LysThrThrValIleLeuAlaPhePheAlaCysTyrPheProTyrTyrValGly 265

Db 805 AAGACCAAGCATCCTCATCTGCTTCTTCCGCTGTTGGCTGCTTACTATCATTTGG 864

QY 266 IleSerIleAspSerPheIleLeuLeuGlyValIleLysGlnGlyCysAspPheGluSer 285

Db 865 ATCAGATCCGACTCTTCATCTCTCCGAAATCATCAAGCAGGCTGTGACTTGAGAAC 924

QY 286 IleValHisLysTyrPheIleSerIleThrGluAlaLeuAlaPhePheHisCysCysLeuAsn 305

Db 925 ACTGTGACAGATGGATTTCATCACCAGAGCCCTAGCTTCTTCACCTGTGTGAC 984

QY 306 ProIleLeuTyrAlaPheLeuGlyAlaLysPheLysSerSerAlaGlnHisAlaLeuAsn 325

Db 985 CCCATCTCTATGCTTCTTCTGAGGCCAATTTAAACCTTGGCCAGCAGCATCACC 1044

QY 326 SerMetSerArgGlySerSerLeuLysIleLeuSerLysGlyLysArgGlyHisSer 345

Db 1045 TCTGTGACAGAGGGTCCAGCTCAAGATCCTCTCCAAAGAAAGCAGGTCGACATTCA 1104

QY 346 SerValSerThrGluSerGluSerSerSerPheHisSerSer 359

Db 1105 TCTGTTCACACTGAGTCTGAGCTTCAAGTTTTCATCCTCCAGC 1146

RESULT 8
US-08-802-627A-3
Sequence 3, Application US/08802627A
Patent No. 5892017
GENERAL INFORMATION:
APPLICANT: Lee, James
APPLICANT: Wood, William I.
TITLE OF INVENTION: NUCLEIC ACID ENCODING PFAA RECEPTOR
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/802,627A
FILING DATE: 19-Feb-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/284586
FILING DATE: 10-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/076093
FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/810782
FILING DATE: 19-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P0706P2P1D2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:
 LENGTH: 1737 base pairs
 TYPE: Nucleic Acid
 STRANDEDNESS: Single
 TOPOLOGY: Linear
 US-08-802-627A-3

Alignment Scores:

Score:	3.29e-188	Length:	1737
Percent Similarity:	1678.50	Matches:	319
Best Local Similarity:	95.48%	Conservative:	19
Query Match:	89.90%	Mismatches:	11
		Indels:	5
		Gaps:	1

US-09-367-052-2 (1-359) x US-08-802-627A-3 (1-1737)

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QY 6 ValSerIleThrSerAspAsnTyrSerGluGluValGlySerGlyAspTyrAspSer 25
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
100 ATCAGTATATACATCTCAGATTAACACACGAGAAATGGCGTACGATGATCC 159
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
QY 26 AsnLysIleuProCysPheArgAspGluAsnValHisPheAsnArgIlePheLeuProThr 45
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
160 ATGAAGGAACCCGCTTCCGTGAGAAATGCTAATTTCATAATAAATCTTCTGCCACC 219
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
QY 46 IleTyrPheIleIlePheLeuThrGlyIleValGlyAsnGlyLeuValIleLeuValMet 65
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
220 ATCTACCTCCATCATCTTCTTAACGCGATGTGGCGAATGGATTGGTCATCTGCTATG 279
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
QY 66 GlyTyrGlnLysLysLeuArgSerMetThrAspLysTyrArgLeuHisLeuSerValAla 85
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
280 GGTTACCAAGAAACTGAGAGACATGACGACACAGACAGGCTGCGCTGCTGAGTGCC 339
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
QY 86 AspLeuLeuPheValIleThrIleuProPheThrAlaValAspIleMetAlaAspTyr 105
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
340 GACCTCCTTTGTCATCAGCGCTTCCCTCTGGCGAGTTAGTGGCGAAACTGGTAC 399
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
QY 106 PheGlyLysPheLeuCysLysAlaValHisIleIleIleTyrThrValAsnLeuTyrSerSer 125
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
400 TTTCGGAACTTCCTCATGCAAGCGCGATGCTCATCTACACAGTCACCTCTACAGCAGT 459
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
QY 126 ValLeuIleLeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThrAsn 145
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
460 GTCTCATCTCCGCTTCATCAGCTGACGCGGACCTGCGCATCTGCGCACCGCCAC 519
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
QY 146 SerGlnArgProArgLysLeuLeuAlaGlyLysAlaValTyrValGlyValTrioIlePro 165
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
520 AGTCAGAGCGCAAGAGAGCTGTGGTGAAAGGTGGTGTGCTGATGGCTGATCCCT 579
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
QY 166 AlaLeuLeuLeuThrIleProAspPheIlePheAlaAspValSerGlnLysAspIleSer 185
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
580 GCCCTCCTGGGACTATTCGCGACTTCATCTTCCCAACGTC-----AGT 624
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
QY 186 GlnGlyAspAspArgTyrIleCysAspArgLeuTyrProAspSerLeuTyrPmetValVal 205
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
625 GAGCAGCATATACATATATCTGTGACCGCTTCCCAATGATGCTGGCTGGCTGTG 684
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
QY 206 PheGlnPheGlnHisIleMetValGlyLeuIleuProGlyIleValIleLeuSerCys 225
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
685 TTCCAGTTTCAAGCACAATGATGTTGGCTTATCTTGGCTGATTTGATCTCTCTCTGC 744
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
QY 226 TyrCysIleIleIleSerLysLeuSerHisSerLysGlnLysGlnLysArgLysAlaLeu 245
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
745 TATTGCAATTATCATCTCCAAAGCTTCACACTCCCAAGGCGCCAGGAAGCGCCCTC 804
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
QY 246 LysThrThrValIleLeuIleLeuAlaPhePheAlaCysTyrPleuProTyrTyrValGly 265
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
805 AAGACCAAGCATCTCATCTCTGCTTCTTCCCTGTTGGCTGCGCTTACTACATTGGG 864
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
QY 266 IleSerIleAspSerPheIleLeuLeuGlyValIleLysGlnLysCysAspPheCys 285
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
865 ATCAGCATCGACTCTTCCTCTCTGAAATCATCAAGCAAGGCTGTGAGTTTGAGAAC 924
  
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QY 286 IleValHisLysTyrPleSerIleThrGluAlaLeuAlaPhePheHisCysCysLeuAsn 305
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
925 ACTGTGACAAAGTGATTTCCATTCACCGAGCCCTTCTTCCACATGTTGTGTAAC 984
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
QY 306 ProIleLeuTyrAlaPheLeuGlyAlaLysPheLysSerSerAlaGlnHisAlaLeuAsn 325
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
985 CCCATCCTCTATCTCTTCTTCTTGGAGCCAAATTTAAACCTCTGCGCACGACGCTCAC 1044
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
QY 326 SerMetSerArgLysSerSerLeuLysIleLeuSerLysGlyLysArgGlyHisSer 345
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
1045 TCTGTGAGCAGAGAGGTTCACGCTTCAGATCTCTCCAAAGAAAGAGAGGTGACATTCA 1104
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
QY 346 SerValSerThrGluSerGluSerSerPheHisSerSer 359
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
1105 TCTGTTCCACGTGAGTCTGATCTTCACGTTTTCACCTCCAGC 1146
  
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RESULT 9

US-08-801-238-3

Sequence 3, Application US/08801238

Patent No. 5919896

GENERAL INFORMATION:

APPLICANT: Lee, James

APPLICANT: Wood, William I.

TITLE OF INVENTION: PFA4 RECEPTOR

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESS: Genentech, Inc.

STREET: 460 Point San Bruno Blvd

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/801,238

FILING DATE: 19-Feb-1997

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/284586

FILING DATE: 10-AUG-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/076093

FILING DATE: 11-JUN-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/810782

FILING DATE: 19-DEC-1991

ATTORNEY/AGENT INFORMATION:

NAME: Love, Richard B.

REGISTRATION NUMBER: 34,659

REFERENCE/DOCKET NUMBER: P0706P2P1D1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415/225-5530

TELEFAX: 415/952-9881

TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 1737 base pairs

TYPE: Nucleic Acid

STRANDEDNESS: Single

TOPOLOGY: Linear

US-08-801-238-3

Alignment Scores:

Pred. No.:	3.29e-188	Length:	1737
Score:	1678.50	Matches:	319
Percent Similarity:	95.48%	Conservative:	19
Best Local Similarity:	90.11%	Mismatches:	11
Query Match:	89.90%	Indels:	5
		Gaps:	1

Db 220 ATCTACTCCATCATCTTCTTAACCTGGCAATGTGGCAATGGATGGTGCATCTGTGCATG 279
QY 66 G1YTYG1LysLysLeuArgSerMetThrAspLysTyrArgLeuHisLeuSerValAla 85
Db 280 GGTACCAAGAACTGAGAACCATGACGACAACTACGAGGCTGACCTGTACGTGACC 339
QY 86 AspLeuLeuPheValIleThrLeuProPheThrAlaValAspAlaMetAlaAspTyrPyr 105
Db 340 GACCTCCTCTTTTCATCAGCGCTCCCTTCTGGGCAATGATCCCTGGCAACCTGTAC 399
QY 106 PheGlyLysPheLeuCysLysAlaValHisIleIleTyrThrValAsnLeuTyrSerSer 125
Db 400 TTTGGGAACCTCTATGCAAGGACGATGCATGTCATCTACACAGTCAACCTCTACACAGT 459
QY 126 ValLeuIleLeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThrAsn 145
Db 460 GTCTCATCTGGCTTTCATCATCTGACGCTGACGCTGACCTGCGCCACGCGCACACAC 519
QY 146 SerGlnArgProArgLysLeuLeuAlaGlyLysAlaValTyrValGlyValTyrPhePro 165
Db 520 AGTCAGAGGCGCAAGAGAGCTGTGGCTGAAGAGGTGTCTATCTTGGCGCTGTGATCCCT 579
QY 166 AlaLeuLeuLeuThrIleProAspPheIlePheAlaAspValSerGlnGlyAspIleSer 185
Db 580 GCCCTCTCTGTGACTATCCCGACTTCATCTTGGCCACAGCTC-----AGT 624
QY 186 GlnGlyAspAspArgTyrIleCysAspArgLeuTyrProAspSerLeuTyrPheValVal 205
Db 625 GAGGCGAGATGACGATATATCTGTGACGCTTCTACCCCAATCACTGTGGGTGTGTG 684
QY 206 PheGlnPheGlnHisIleMetValGlyLeuIleLeuProGlyIleValIleLeuSerCys 225
Db 685 TTCAGATTCAGACATCATAGTGTGGCCTTATCTGCGTGTATCTGATCCCTGTCTCG 744
QY 226 TyrCysIleIleIleSerLysLeuSerHisSerLysGlyHisGlnLysArgLysAlaLeu 245
Db 745 TATTCATTATATCTCCCAAGCTGTACACTCCAAAGGCGCACCAAGGCGCAAGGCGCTC 804
QY 246 LysThrThrValIleLeuIleLeuAlaPhePheAlaCysThrLeuProTyrTyrValGly 265
Db 805 AAGACCAACATCATCTCATCTCGGCTTCTTCTGCTGTGGCTGCTTACTGATTTGGG 864
QY 266 IleSerIleAspSerPheIleLeuLeuGlyValIleLysGlnGlyCysAspPheGlnSer 285
Db 865 ATCAGCATGACATCTTCATCTCTGGAATATCATCAAGCAAGGAGTGTGAGAAC 924
QY 286 IleValHisLysTyrPheSerIleThrGlnAlaLeuAlaPhePheHisCysCysLeuAsn 305
Db 925 ACTGTGCACAAAGTGGATTTCCATCACCGAGGCCCTGTCTTCTTCACATGTTGTCGAAC 984
QY 306 ProIleLeuTyrAlaPheLeuGlyAlaLysPheLysSerSerIleGlnHisAlaLeuAsn 325
Db 985 CCCATCTCTATCTTCTTCTTGGAGCCAAATTTAAACCTCTGCGCCAGCAGCATCTCAC 1044
QY 326 SerMetSerArgLysSerSerLeuLysIleLeuSerLysGlyLysArgLysGlyHisSer 345
Db 1045 TCTGTAGACAGAGGAGGCTCAAGATCCCTCTCCAAAGGAAGGAGAGTGTGACATTTCA 1104
QY 346 SerValSerThrGlnSerLysSerSerSerPheHisSerSer 359
Db 1105 TCTGTTTCCACATGAGTGTGATCTTCAAGTTTCACTCCAGC 1146

RESULT 11
US-09-104-296-3
Sequence 3, Application US/09104296
Patent No. 6087475
GENERAL INFORMATION:
APPLICANT: Lee, James
APPLICANT: Wood, William I.
TITLE OF INVENTION: PEA4 Receptors
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way
City: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/104,296
FILING DATE: 24-June-1998
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/701265
FILING DATE: 22-AUG-1996
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/664228
FILING DATE: 06-JUN-1996
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/076093
FILING DATE: 11-JUN-1993
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/810762
FILING DATE: 19-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P0706P2C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1737 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
US-09-104-296-3
Alignment Scores:
Pred. No.: 3,296-188 Length: 1737
Score: 1678.50 Matches: 319
Percent Similarity: 95.488 Conservative: 19
Best Local Similarity: 90.118 Mismatches: 11
Query Match: 89.904 Indels: 5
DB: 3 Gaps: 1
US-09-367-052-2 (1-359) x US-09-104-296-3 (1-1737)
QY 6 ValSerIleTyrThrSerAspAsnTyrSerGluGluValGlySerGlyAspTyrAspSer 25
Db 100 ATCAGATATATACATCTCAAGATTAACACCGAGAAATGCGCTCAGGAGATATGACTCC 159
QY 26 AsnLysGlnProCysPheArgGArgLysAsnValHisPheAsnArgIlePheLeuProThr 45
Db 160 ATGAGGAAACCCGTGTTCCGTGAGAAATGCTTAATTTCAATAATTAATTTCTGCGCCAC 219
QY 46 IleTyrPheIleIlePheLeuThrGlyIleValGlyAsnGlyLeuValIleLeuValMet 65
Db 220 ATCTACTCCATCATCTTCTTAACCTGGCATTTGGGCAATGATGGTGTATCTCTGTGTCATG 279
QY 66 G1YTYG1LysLysLeuArgSerMetThrAspLysTyrArgLeuHisLeuSerValAla 85
Db 280 GGTACCAAGAAACTGAGAACCATGACGACAACTACGAGGCTGACCTGTACGTGACC 339
QY 86 AspLeuLeuPheValIleThrLeuProPheThrAlaValAspAlaMetAlaAspTyrPyr 105
Db 340 GACCTCCTCTTTTCATCAGCGCTCCCTTCTGGGCAATGATCCCTGGCAACCTGTAC 399
QY 106 PheGlyLysPheLeuCysLysAlaValHisIleIleTyrThrValAsnLeuTyrSerSer 125

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      400 TTTGGGAACCTCCATATCAAGGAGCCAGTCATCATACACAGTCAACCTCTACAGCAGT 459
      126 ValLeuLeuLeuAlaPheLeuSerLeuAspArgTyrLeuAlaIleValHisAlaThrAsn 145
      460 GTCTCTATCCCTGGCGCTTATCATAGTCTGACCGCTTACCTGGCCATCGCCACGACCAAC 519
      146 SerGlnArgProAlaGlySerLeuLeuAlaGluLysAlaValTyrValGlyValTyrIlePro 165
      520 AGTACAGAGCCCAAGAGAGCTGTGGCTGAAAAGGTGCTATGTGGCGCTGGATCCCT 579
      166 AlaLeuLeuLeuThrIleProAspPheIlePheAlaAspValSerGlnGlyAspIleSer 185
      580 GCCCTCCCTGGAGACTATCCCGACTCATCTCTTCCCAACGTC-----AGT 624
      186 GlnGlyAspAspArgTyrIleCysAspArgLeuTyrProAspSerLeuTyrPheValVal 205
      625 GAGGCAAGATGACAGATATATCTGTGACCGCTTCAACCCCAATGACTGTGGGTGGTGTG 684
      206 PheGlnPheGlnHisIleMetValGlyLeuIleLeuProGlyIleValIleLeuSerCys 225
      685 TTCCAGTTTACGACATCATGAGTGGGCTTATCTGCTGCTATTTGTCATCTCTCTGC 744
      226 TyrCysIleIleIleSerLysLeuSerHisSerLysGlnGlyAspArgLysAlaLeu 245
      745 TATGCAATATATCATCTCCAAAGCTGTCACTCAAGGAGCCACAGAAAGCCAGAGCCCTC 804
      246 LysThrThrValIleLeuIleLeuAlaPhePheAlaCysTyrPheProTyrTyrValGly 265
      805 AAGGCCACAGTCACTCATCTGCTGCTTCTTCCCTGCTGGCCCTTACTATCAATTCAG 864
      266 IleSerIleAspSerPheIleLeuLeuGlyValIleLysGlnGlyCysAspPheGluSer 285
      865 ATGACGATTCAGCTCTCTCATCTCTCTGGAATCATCAAGCAAGGCTGTGATTTGAGAAC 924
      286 IleValHisIleTyrPheIleSerIleThrGluAlaLeuAlaPhePheHisCysCysLeuAsn 305
      925 ACTGTGCAACAAGTGGATTCATCCATCAGCAGGCGCTTACTTCTCCACTGTGTGCTGAC 984
      306 ProIleLeuTyrAlaPheLeuGlyAlaLysPheLysSerSerAlaGlnHisAlaLeuAsn 325
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SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/06380
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/076093
FILING DATE: 11-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 706P2P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1737 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
PCT-US94-06380-2

Alignment Scores:
Pred. NO.: 3,29e-188 Length: 1737
Score: 1678.50 Matches: 319
Percent Similarity: 95.48% Conservative: 19
Best Local Similarity: 90.11% Mismatches: 11
Query Match: 89.90% Indels: 5
DB: Gaps: 1

US-09-367-052-2 (1-359) x PCT-US94-06380-2 (1-1737)
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      160 ATGAGAGAAACCTGTTCCGTGAAGAAATGCTTAATTAATAATCTTCTCCACACC 219
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      220 ATCTACCTCATCATCTCTTACTAGCTGCGATTTGGGCAATGGATTTGCTCATCTGCTATG 279
      66 GlyTyrGlnLysLysLeuArgSerMetThrAspLysTyrArgLeuHisLeuSerValAla 85
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      86 AspLeuLeuPheValIleThrLeuProPheTyrPalaValAspAlaMetAlaAspTyr 105
      340 GACCTCTCTTTCATCAGCTCCCTTGGGCACTGTGATGCCGCGCAAACTGGTATC 399
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      146 SerGlnArgProAlaGlySerLeuLeuAlaGluLysAlaValTyrValGlyValTyrIlePro 165
      520 AGTACAGAGCCCAAGAGAGCTGTGGCTGAAAAGGTGCTATGTGGCGCTGGATCCCT 579
      166 AlaLeuLeuLeuThrIleProAspPheIlePheAlaAspValSerGlnGlyAspIleSer 185
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Db 1170 TCTGTTTCCACTGAGTGTGAGTCTTCAAGTTTCACTTCCAGC 1211

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UNT 14
9-299-843A-45
Sequence 45, Application US/09299843A
Patent No. 6107475
GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
TITLE OF INVENTION: No. 6107475el Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESS: Marshall, O'Toole, Gerstein, Murray &
ADDRESS: Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/299,843A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/088,337
FILING DATE: 01-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/153,848
FILING DATE: 17-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Jill E. Uhl
REGISTRATION NUMBER: 43,213
REFERENCE/DOCKET NUMBER: 27866/320598
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX:
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 1317 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 201..1211

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US-09-299-843A-45
Alignment Scores:
Pred. No.: 1,11e-187 Length: 1317
Score: 1672.50 Matches: 318
Percent Similarity: 95.20% Conservative: 19
Best Local Similarity: 89.83% Mismatches: 12
Query Match: 89.58% Indels: 5
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Db 1170 TCTGTTCACACTGAGTGTGAGTCTTCAAGTTTTCACCTCCAGC 1211

RESULT 15

US-09-088-337B-45
Sequence 45, Application US/09088337B
Patent No. 6348574

GENERAL INFORMATION:

APPLICANT: Godiska, Ronald
Gray, Patrick W.
Schweikart, Vicki L.
TITLE OF INVENTION: No. 6348574el Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
Botun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/088,337B
FILING DATE: 01-Jun-1998
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/153,848
FILING DATE: 17-NOV-1993
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 6348574and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31794
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448

INFORMATION FOR SEQ ID NO: 45:

SEQUENCE CHARACTERISTICS:
LENGTH: 1317 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA

FEATURE:
NAME/KEY: CDS
LOCATION: 201..1211
SEQUENCE DESCRIPTION: SEQ ID NO: 45:
US-09-088-337B-45

Alignment Scores:

Pred. No.: 1,11e-187 Length: 1317
Score: 1672.50 Matches: 318
Percent Similarity: 95.20% Conservative: 19
Best Local Similarity: 89.83% Mismatches: 12
Query Match: 89.58% Indels: 5
DB: 4 Gaps: 1

US-09-367-052-2 (1-359) x US-09-088-337B-45 (1-1317)

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Mon Jul 14 09:29:48 2003

us-09-367-052-2.rni

Page 15

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Job time : 67 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

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Perfect score: 1867

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Searched: 1105431 segs, 789497651 residues

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	1678.5	89.9	1679	US-10-225-567A-75
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4	1670.5	89.5	1102	US-09-870-759-143

5	1139	61.0	1902	US-09-953-692-1	Sequence 1, Appl1
6	1139	61.0	1902	US-09-953-717-1	Sequence 1, Appl1
7	657.5	35.2	421	US-09-796-682-2611	Sequence 2611, Ap
8	657.5	35.2	421	US-10-040-862-2611	Sequence 2611, Ap
9	584	31.3	1107	US-10-251-385-19	Sequence 19, Appl
10	584	31.3	1670	US-10-225-567A-73	Sequence 73, Appl
11	584	31.3	1670	US-09-880-107-3833	Sequence 3833, Ap
12	580	31.1	1107	US-10-251-385-173	Sequence 173, Ap
13	575	30.8	1877	US-10-106-688-2125	Sequence 1215, Ap
14	570.5	30.6	1607	US-10-120-394-19	Sequence 19, Appl
15	570.5	30.6	1607	US-09-764-413-19	Sequence 19, Appl
16	570.5	30.6	1677	US-10-225-567A-65	Sequence 65, Appl
17	570.5	30.6	1677	US-09-837-446-1	Sequence 1, Appl1
18	555	29.7	1068	US-10-237-563-47	Sequence 47, Appl
19	552	29.6	1068	US-10-237-563-48	Sequence 48, Appl
20	549.5	29.4	1068	US-10-237-563-41	Sequence 41, Appl
21	549.5	29.4	1068	US-10-237-563-43	Sequence 43, Appl
22	549	29.4	1068	US-10-237-563-42	Sequence 42, Appl
23	546	29.2	1068	US-10-237-563-45	Sequence 45, Appl
24	544.5	29.2	1068	US-10-237-563-38	Sequence 38, Appl
25	544.5	29.2	1068	US-10-237-563-39	Sequence 39, Appl
26	544.5	29.2	1068	US-10-225-567A-385	Sequence 385, Ap
27	543.5	29.1	1068	US-10-237-563-46	Sequence 46, Appl
28	542.5	29.1	1053	US-10-237-563-40	Sequence 40, Appl
29	541.5	29.0	1068	US-10-237-563-44	Sequence 44, Appl
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38	537.5	28.8	2139	US-10-225-567A-67	Sequence 67, Appl
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40	534	28.6	1074	US-10-251-385-23	Sequence 23, Appl
41	534	28.6	2462	US-10-225-567A-240	Sequence 240, Ap
42	534	28.6	2577	US-09-966-755-1	Sequence 1, Appl1
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ALIGNMENTS

RESULT 1
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Sequence 2143, Application US/09880107
Patent No. US20020142981A1
GENERAL INFORMATION:
APPLICANT: Horne, Darcil T.
APPLICANT: Vockley, Joseph G.
APPLICANT: Scherf, Uwe
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
FILE REFERENCE: 44921-5028-WO
CURRENT FILING DATE: 2001-06-14
PRIOR FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2143
LENGTH: 1670
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Genbank Accession No. US20020142981A1 L06797
US-09-880-107-2143
Alignment Scores:

Pred. No.: 3,31e-182 Length: 1670
 Score: 1678.50 Matches: 319
 Percent Similarity: 95.48% Conservative: 19
 Best Local Similarity: 90.11% Mismatches: 11
 Query Match: 89.90% Indels: 5
 Gaps: 1

US-09-367-052-2 (1-359) x US-09-880-107-2143 (1-1670)

```

Oy 6 ValSerIleTyrThrSerAspAsnTyrSerGluGluValAlaGlySerGlyAspTyrAspSer 25
Db 82 ATCGATTAATACCTTACAGATTAACATACCGAAGAAATGGGCTCAGGGACATAGACTCC 141
Oy 26 AsnysGluProCysPheArgAspGluAsnValHisPheAsnArgIlePheLeuProThr 45
Db 142 ATGAGAGAACCCCTTTCCGTAAGAAATGCTTAATTCATATAAATCTTCTCCACC 201
Oy 46 IleTyrPheIleIlePheLeuThrGlyIleValGlyAsnGlyLeuValIleLeuValMet 65
Db 202 ATCTACTCCATCATCTTCTTAACCTGGCATTTGCGCAATGGATTTGGTCACTCCGTCATG 261
Oy 66 GlyTyrGlnLysLysLeuArgSerMetThrAspLysTyrArgLeuHisLeuSerValAla 85
Db 262 GGTTCACGAGAAAGACTGAGAGCATGACGACAAAGTACAGGCTGCACCTGTCACTGGCC 321
Oy 86 AspleuLeuPheValIleThrLeuProPheTyrPheValAlaAspAlaMetAlaAspTyr 105
Db 322 GACCTCCTCTTTGTCATCAGCCTTCTCTGCGCACTGTAGTCCGCGGCAAACTGGTAC 381
Oy 106 PheGlyLysPheLeuCysLysAlaValHisIleIleTyrThrValAsnLeuTyrSerSer 125
Db 382 TTTGGGAACCTTCTTAACGAGGAGCTCATGCTACACAGTCAACCTTACAGCAGT 441
Oy 126 ValLeuIleLeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThrAsn 145
Db 442 GTCTCTACCTCGGCTTCATAGTCTGACCGCTACCTGGCCATGCTCCAGCCAGCAAC 501
Oy 146 SerGlnArgProArgLysLeuLeuAlaGluLysAlaValTyrValGlyValTyrPhePro 165
Db 502 AGCTAGAGGCCAAGAGAGCTGTGGCGAAGAGTGTCTATGTGGCGTGTGGATCCT 561
Oy 166 AlaLeuLeuLeuThrIleProAspPheIlePheAlaAspValSerGlnGlyAspIleSer 185
Db 562 GCCCTCTGCTGACTATTTCCGACTCATCTTCCCAACGATC-----AGT 606
Oy 186 GlnGlyAspAspArgTyrIleCysAspArgLeuTyrProAspSerLeuTyrPheValVal 205
Db 607 GAGGACATGACATATATCTGTGACCGCTTCAACCCCAATGACTGTGGGTGTGTG 666
Oy 206 PheGlnPheGlnHisIleMetValGlyLeuLeuProGlyIleValIleLeuSerCys 225
Db 667 TTTCAGTTTCAGACATCATGTTGGCTTATCTGCTGATTTGATCATCTTCTCCGTC 726
Oy 226 TyrTyrIleIleIleSerLysLeuSerHisSerLysGlyHisGlnLysAlaGlyAlaLeu 245
Db 727 TATTGCAATTATCATCTCCAACTGTCAACACCAAGGCCCAAGAGCGGAGCCCTC 786
Oy 246 LysThrThrValIleLeuIleLeuAlaPhePheIleAspTyrPheValGly 265
Db 787 AAGACCAAGTCACTCATCTGCTTCTTCCCTGTGGCTTCTTACTTAATTTGGG 846
Oy 266 IleSerIleAspSerPheIleLeuLeuGlyValIleLysGlnGlyCysAspPheGluSer 285
Db 847 ATCAGCATCGACTCTTCATCTCTCTGGAATCATCAAGCAAGGCTTGAGATTGAGAC 906
Oy 286 IleValHisLysTyrPheSerIleThrGluAlaLeuAlaPhePheHisCysCysLeuAsn 305
Db 907 ACTGTGCAAGTGGATTTCATCACCAGAGCCCTAGCTTTCTTCCACTGTTGTCTGAAC 966
Oy 306 ProIleLeuTyrAlaPheLeuGlyAlaLysPheLysSerSerAlaGlnHisAlaLeuAsn 325
Db 967 CCCATCTCTATGCTTTCCTTGGAGCCAAATTTAAACCTTGCCAGCAGCAGCTCACC 1026
  
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Oy 326 SerMetSerArgLysSerSerLeuLysIleLeuSerLysGlyAsnArgGlyGlnHisSer 345
 Db 1027 TCTGTGAGCAGAGGCTCCACCTCAGATCTCTCCAAAGAAAGGAGTGGACATTTCA 1086
 Oy 346 SerValSerThrGluSerGluSerSerPheHisSerSer 359
 Db 1087 TCTGTTTCCACTGAGTCTGAGTCTTCAAGTTTTCACCTCAGC 1128

RESULT 2

```

US-10-225-567A-75
: Sequence 75, Application US/10225567A
: Publication No. US20030113798A1
: GENERAL INFORMATION:
: APPLICANT: Lifespan Biosciences
: APPLICANT: Brown, Joseph P.
: APPLICANT: Burner, Glenn C.
: APPLICANT: Roush, Christine L.
: TITLE OR INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPT
: FILE REFERENCE: 1920-4-4
: CURRENT APPLICATION NUMBER: US/10/225,567A
: PRIOR FILING DATE: 2001-12-19
: PRIOR APPLICATION NUMBER: 60/257,144
: NUMBER OF SEQ ID NOS: 292
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 75
: LENGTH: 1679
: TYPE: DNA
: ORGANISM: Homo sapiens
US-10-225-567A-75
  
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Alignment Scores:

Pred. No.: 3,33e-182 Length: 1679
 Score: 1678.50 Matches: 319
 Percent Similarity: 95.48% Conservative: 19
 Best Local Similarity: 90.11% Mismatches: 11
 Query Match: 89.90% Indels: 5
 Gaps: 1

US-09-367-052-2 (1-359) x US-10-225-567A-75 (1-1679)

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Oy 6 ValSerIleTyrThrSerAspAsnTyrSerGluGluValAlaGlySerGlyAspTyrAspSer 25
Db 98 ATCAGTATTAATACCTTACAGATTAACATACCGAAGAAATGGGCTCAGGGACATAGACTCC 157
Oy 26 AsnysGluProCysPheArgAspGluAsnValHisPheAsnArgIlePheLeuProThr 45
Db 158 ATGAGAGAACCCCTTTCCGTAAGAAATGCTTAATTCATATAAATCTTCTCCACC 217
Oy 46 IleTyrPheIleIlePheLeuThrGlyIleValGlyAsnGlyLeuValIleLeuValMet 65
Db 218 ATCTACTCCATCATCTTCTTAACCTGGCATTTGCGCAATGGATTTGGTCACTCCGTCATG 277
Oy 66 GlyTyrGlnLysLysLeuArgSerMetThrAspLysTyrArgLeuHisLeuSerValAla 85
Db 278 GGTTCACGAGAAAGACTGAGAGCATGACGACAAAGTACAGGCTGCACCTGTGAGGCC 337
Oy 86 AspleuLeuPheValIleThrLeuProPheTyrPheValAlaAspAlaMetAlaAspTyr 105
Db 338 GACCTCCTCTTTGTCATCAGCCTTCTCTGCGCACTGTAGTCCGCGCAAACTGGTAC 397
Oy 106 PheGlyLysPheLeuCysLysAlaValHisIleIleTyrThrValAsnLeuTyrSerSer 125
Db 398 TTTGGGAACCTTCTTAATCAGAGCGCTGCATGCTATCAACAGTCAACCTTACAGCAGT 457
Oy 126 ValLeuIleLeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThrAsn 145
Db 458 GTCTCTACCTCGGCTTCATCAGTCTGACCGCTACCTGGCCATGCTCCAGCCAGCAAC 517
Oy 146 SerGlnArgProArgLysLeuLeuAlaGluLysAlaValTyrValGlyValTyrPhePro 165
Db 518 AGTCAGAGGCCAAGAGAGCTGTGGCGAAGAGTGTCTATGTTGGCGTGTGGATCCT 577
  
```


QY 226 TyrCysIleIleIleIleSerLysLeuSerHisSerLysGlyHisGlnLysArgLysAlaLeu 245
|||||
Db 745 TATTGATATATCTATCTCCAGCTGCTACACTCCAAAGGACCAGAGGAGGAGGCCCTC 804
QY 246 LysThrThrValIleLeuIleLeuAlaPhePheAlaCysTrpPheProTyrTrpValGly 265
|||||
Db 805 AAGACACAGTATCTCTCATCTCGGCTTCTTGCTGCTGCTGCTGCTTACTCATTTGGG 864
QY 266 IleSerIleAspSerPheIleLeuLeuGlyValIleLysGlnGlyCysAspPheGlySer 285
|||||
Db 865 ATCAGATGAGACCTTCATCTCCCTGGAATCATCAAGCAAGGAGGTGATTTGAGAAC 924
QY 286 IleValIleLysTrpIleSerIleThrGluAlaLeuAlaPhePheHisCysCysLeuAsn 305
|||||
Db 925 ACCTGTCACAGAGGATTTCCATCCACCGAGGCCCTTCTTCCACTGTTCTTGAAAC 984
QY 306 ProIleLeuTyrAlaPheLeuGlyAlaLysPheLysSerSerAlaGlnHisAlaLeuAsn 325
|||||
Db 985 CCCATCTCTATCTCTTCTTCCCTTGAGCCAAATTTAAACCTCTCCACAGCAGCCTCACC 1044
QY 326 SerMetSerArgLysSerLysSerLysIleLeuSerLysGlyLysArgGlyHisSer 345
|||||
Db 1045 TCTGTAGCAGAGGAGGTCCAGCTCAAGATCTCTCCAAAGGAAGGAGGTGACATTGA 1104
QY 346 SerValSerThrGluSerGluSerSerPheHisSerSer 359
|||||
Db 1105 TCTGTTCCACGTGAGTCTGAGTTCATCAAGTTTCCACTCCAGC 1146

RESULT 4

US-09-870-759-143
; Sequence 143, Application US/09870759
; Patent No. US2002017751A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 870759
; CURRENT APPLICATION NUMBER: US/09/870,759
; PRIOR FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/208,128
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 143
; LENGTH: 1102
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (44)..(1102)
; OTHER INFORMATION:
US-09-870-759-143

Alignment Scores:

Score: 1,43e-181 Length: 1102
Pred. No.: 1670.50 Matches: 317
Percent Similarity: 95.20% Conservative: 20
Best Local Similarity: 89.55% Mismatches: 12
Query Match: 89.48% Indels: 5
DB: 9 Gaps: 1

US-09-367-052-2 (1-359) x US-09-870-759-143 (1-1102)

QY 6 ValSerIleTyrThrSerAspAsnTyrSerGluGluValGlySerGlyAspTyrAspSer 25
|||||
Db 53 ATCAGATATATCTCTCAGTATACCTACCGAGGAATGGGCTCAGAGGAGCTATGACTCC 112
QY 26 AsnLysGluProCysPheArgAspGluAsnValHisPheAsnArgIlePheLeuProThr 45
|||||
Db 113 ATGAGAGAACCGCTTTCGCTGAGAAATGCAATTTCAATAAATCTTCCGCCACAC 172
QY 46 IleTyrPheIleIlePheLeuThrGlyIleValGlyAsnGlyLeuValIleLeuValMet 65
|||||

Db 173 ATCTACTCCATCATCTTTTAACGTGCAATGTGGCAATGATGGTCACTCCGTGCATG 232
QY 66 GlyTyrGlnLysLysLeuArgSerMetThrAspLysTyrArgLeuHisLeuSerValAla 85
|||||
Db 233 GGTTCACAGAAAGAAATGGAAGCAATGAGGACAGCAATGAGGCTGACCTGTCAGTGGCC 292
QY 86 AspLeuLeuPheValIleThrLeuProPheTrpAlaValAspAlaMetAlaAspTrpTyr 105
|||||
Db 293 GACCTCTCTTTGTATCATCAGCTTCCCTTCTGAGGAGTGTGATGCCGTGCAACACTGTAC 352
QY 106 PheGlyLysPheLeuCysLysAlaValHisIleIleTyrThrValAsnLeuTyrSerSer 125
|||||
Db 353 TTTGGAACTTCTCTATGACAGGACAGTCCATGTCATCTACACAGTCAACCTCTACAGCACT 412
QY 126 ValLeuIleLeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThrAsn 145
|||||
Db 413 GTCTCATCTCTGAGCTTCATCAGTGGAGCCCTTACCTGCGCATTTGTCACGCCACACAC 472
QY 146 SerGlnArgProArgLysLeuLeuAlaGlyLysAlaValTyrValGlyValTrpIlePro 165
|||||
Db 473 AGTCAGAGGCCAAGAGAGCTGTGGCTGAAAGGTGTCTATGTGGCGCTCGATCCCT 532
QY 166 AlaLeuLeuLeuThrIleProAspPheIlePheAlaAspValSerGlnGlyAspIleSer 185
|||||
Db 533 GCCCTCTCTGACTATCTCCGACTTCATCTTTCGCAAGCTC-----AGT 577
QY 186 GlnGlyAspAspArgTyrIleCysAspArgLeuTyrProAspSerLeuTrpMetValVal 205
|||||
Db 578 GAGGACGATGACAGATATATCTGTGACCCCTTACCCCAATGACTGTGGGTGTTGTG 637
QY 206 PheGlnPheGlnHisIleMetValGlyLeuIleLeuProGlyIleValIleLeuSerCys 225
|||||
Db 638 TTCAGATTCACAGACATCATGTGTGGCTTATCTCCCTGATGATGTATCTCTGCTCC 697
QY 226 TyrCysIleIleIleSerLysLeuSerHisSerLysGlyHisGlnLysArgLysAlaLeu 245
|||||
Db 698 TATTGATATATCATCTCCAGGCTGTCCACTCCAAAGGACCAGAGGAGGCCCTC 757
QY 246 LysThrThrValIleLeuIleLeuAlaPhePheAlaCysTrpLeuProTyrTrpValGly 265
|||||
Db 758 AAGACCACAAATCATCTCCATCTCTGCTTCTTCTGCTGTGGCTGCTTACTCATTTGGG 817
QY 266 IleSerIleAspSerPheIleLeuLeuGlyValIleLysGlnGlyCysAspPheGlySer 285
|||||
Db 818 ATCAGCATGAGCTCTTCATCTCTCCGAAATCATCAACAGAGGAGTGTGAGAAC 877
QY 286 IleValHisLysTrpIleSerIleThrGluAlaLeuAlaPhePheHisCysCysLeuAsn 305
|||||
Db 878 ACTGTGCACAGGTGATTCATCCATCCAGGAGGCCCTAGCTTCTTCCACTGTTGTGAAAC 937
QY 306 ProIleLeuTyrAlaPheLeuGlyAlaLysPheLysSerSerAlaGlnHisAlaLeuAsn 325
|||||
Db 938 CCCATCTCTATGCTTCTTCTTGAGCCAAATTTAAACCTCTGCGCAGCAGCAGCCTCACC 997
QY 326 SerMetSerArgLysSerLysSerLysIleLeuSerLysGlyLysArgGlyHisSer 345
|||||
Db 998 TCTGTAGCAGAGGAGGTCCAGCTCAAGATCTCTCCAAAGGAAGGAGGTGACATTGCA 1057
QY 346 SerValSerThrGluSerGluSerSerPheHisSerSer 359
|||||
Db 1058 TCTGTTCCACGTGAGTCTGAGTTCATCAAGTTTCCACTCCAGC 1099

RESULT 5

US-09-953-692-1
; Sequence 1, Application US/09953692
; Patent No. US20020107195A1
; GENERAL INFORMATION:
; APPLICANT: Shalley, Gupta K.
; TITLE OF INVENTION: Method for Inducing Chemotaxis in Endothelial Cells by
; FILE REFERENCE: P50676C1
; CURRENT APPLICATION NUMBER: US/09/953,692
; CURRENT FILING DATE: 2001-09-17

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PRIOR APPLICATION NUMBER: 09/358,624
PRIOR FILING DATE: 1999-07-21
PRIOR APPLICATION NUMBER: 60/093,596
PRIOR FILING DATE: 1998-07-21
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1
LENGTH: 1902
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: unsure
LOCATION: (158)(223)(225)(226)(335)(466)(520)(530)(645)(763)(825)(1120)
LOCATION: (1183)
US-09-953-692-1

Alignment Scores:
Pred. No.: 2,71e-120 Length: 1902
Score: 1139.00 Matches: 307
Percent Similarity: 75.41% Conservative: 18
Local Similarity: 71.23% Mismatches: 23
Identity Match: 61.01% Indels: 88
Gaps: 21

US-09-367-052-2 (1-359) x US-09-953-692-1 (1-1902)

OY 7 SerIleYrThrSerAspAsnTyrSerGluGluValIGlySerGlyAspTyr----- 23
Db 103 AGTATATACACTTTCGATACACTACCCAGAAATGGGCTCAGGGAGACTA-SYTSNDNTM 161
OY 24 -----AspSerAsnLysGluProCysPheArgAspGluAsnValHisPheAsn----- 39
Db 162 GSGDYTAGCTCATGAAGAACCCCTGTTCCGTGAAGAAATGCTAATTCAATDMSKC 221
OY 40 ----ArgIlePheLeuProThrIleYrPheIleIlePheLeuThrGlyIleVal----- 56
Db 222 RNANNAATCTTCCCTGCCACCACCTACTCCATCTCTTCACTTCACTGGCATTGTCTYST 281
OY 57 --GlyAsnGlyLeuValIleLeuValIleMetGlyTyrGlyLysLysLeuArg----- 72
Db 282 GVGGAATGGATGGTGCATCCCTGGTCATGGGTTACCAGAGAACTGAGAGAGNGVWGY 341
OY 73 --SerMetThrAspLysTyrArgLeuHisLeuSerValAlaAspLeuPheVal----- 90
Db 342 KKRSCATGACGAGCAAGTACAGCGTCACCTGTGAGCCGACCTCTTGM-TDKY 400
OY 91 ----IleThrLeuProPheTrpAlaValAspAlaMetLysPrtPyrPhe----- 106
Db 401 RHSAVDGATCATCGCTTCCCTTCTGGGCAGTGATGCGCGTGGCAAACTGGTACTTTVWA 460
OY 107 -----GlyLysPheLeuCysLysAlaValHisIleIleYrThrValAsnLeu----- 122
Db 461 VDAVANWVGGAACCTTCTATCCAAAGGCAAGTCCATGCTCTTCAACAGTCAACCTCTAGN 520
OY 123 -----TyrSerSerValLeuIleLeuAlaPheIleSerLeuAspArgTyrLeuAla 139
Db 521 CKAHVHTVNCACAGAGTCTCTCATCGCGCTTCATCAGTGTGACCGCATACCTGGCG 580
OY 140 ----IleValHisAlaThrAsnSerGlnArgProArgLysLeuLeuAlaGlyLys 156
Db 581 ASSVASDRATCTCGACGCCCAACAGTCAAGAGGCCAAAGAACTGTGGCTGAAAG 640
OY 157 Ala-----ValTyrValGlyValTrpIleProAlaLeuLeuThrIle--Pr 172
Db 641 VA-ATNSRRKAKGTGTCTATGTGGCGTGTGATCCCTGCTCTGTGCTATTTCC 699
OY 172 O-----AspPheIlePheAlaAspValSerGlnGlyAspIleSerGlnGlyAspAs 189
Db 700 GAVVTVGVWATDCTTCATCTTGGCAAGCTC-----AGTGAAGCAGATGA 744
OY 189 pArgTyrIleCysAspArg-----LeuTyrProAspSerLeuTyrMetValVa 205
Db 745 CAGATATATCTGTGACCA-NWSADRDYCDGCTTCAACCCCAATGACTGTGGTGTCT 803

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OY 205 lPheGlnPheGlnHisIle-----MetValGlyLeuIleLeuProGlyIleValI1 222
Db 804 GTTCCAGTTTCAGCAGCATRNYDWWVHATGGTTGGCTTATCCGCGCATTTGTCTAT 863
OY 222 eLeuSerCysTyrCysIle-----IleIleSerLysLeuSerHisSerLysGlyH1 239
Db 864 CCTGTCTCTCTATTCATTCATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTC 923
OY 239 sGlnLysArgLysAla-----LeuLysThrTrpValIleLeuIleLeuAlaPhe 255
Db 924 CCAGAAAGGCGAAGGCCCSKSHKGRKATCAAGACACAGTATCTATCTGCTT 983
OY 255 ePheAlaCysTrpLeuPro-----TyrTrpValGlyIleSerIleAspSerPheIle 272
Db 984 CTTCGCTCTGTGGCTGCTCTCTTVAACWATCTCATTTGGATAGCATGCATCTTCTATC 1043
OY 273 LeuLeuGlyValIleLys-----GlnGlyCysAspPheGlnSerIleValHisLysTr 290
Db 1044 CTCTGGAATATCATCAAAAYGSDSKGCAAGGCTGTGAGTGTGAGAACACTGCACAAAGT 1103
OY 290 pIleSerIleThr-----Glu-AlaLeuAlaPhePheHisCysCysLeuAsnProI 307
Db 1104 GATTTCCATCACCGGCGCNTVHKWSTAGGCCCTTCTTCCACTGTGTCTGAACCCCA 1163
OY 307 lLeuTyrAlaPhe-----LeuGlyAlaLysPheLysSerSerAlaGlnHisAlaL 324
Db 1164 TCTCTATTC-TTTCACAHCCNACTTTGGAGCCAAATTTAAACCTCTGCCCGCACGAC 1222
OY 324 eAsnSerMet-----SerArgGlySerSerLeuLysIleLeuSerLysGly 339
Db 1223 TCACCTCTGTGAGGAKRTSAHATSVSCAGAGGCTCAGGCTCCTCTCCAAAGGA 1282
OY 340 LysArgGlyGlyHis-----SerSerValSerThrGlnSerGlnSerSer 355
Db 1283 AAGCAGAGTGGACATTGSSSKSKGRGHCATCTGTTCCACTGAGTGTGAGTCTTCAAG 1342
OY 355 rPheHisSerSer 359
Db 1343 TTTTCACTCCAGC 1355

RESULT 6
US-09-953-717-1
; Sequence 1, Application US/09953717
; Patent No. US20020107196A1
; GENERAL INFORMATION:
; APPLICANT: Shalley, Gupta K.
; TITLE OF INVENTION: Method for Inducing Chemotaxis in Endothelial Cells by
; FILE REFERENCE: P50676D1
; CURRENT APPLICATION NUMBER: US/09/953,717
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: 09/358,624
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: 60/093,596
; PRIOR FILING DATE: 1998-07-21
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1902
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (158)(223)(225)(226)(335)(466)(520)(530)(645)(763)(825)(1120)
; LOCATION: (1183)
US-09-953-717-1

Alignment Scores:
Pred. No.: 2,71e-120 Length: 1902
Score: 1139.00 Matches: 307
Percent Similarity: 75.41% Conservative: 18
Best Local Similarity: 71.23% Mismatches: 23

```

Query Match: 61.01% Indels: 88
 DB: 10 Gaps: 21
 US-09-367-052-2 (1-359) x US-09-953-717-1 (1-1902)

OY 7 SerIleYrThrSerAspAsnYrSerGluValGlySerGlyAspTyr----- 23
 |||||
 DB 103 AGTATATACCTTCAGATACTACACCGAAGAAATGGCTCAGGGAGCTA-SYTSNDYTM 161
 OY 24 -----AspSerAsnLysGluProCysPheArgAspGluAsnValHisPheAsn----- 39
 |||||
 DB 162 GSGDYTCCTCATGACGAACCCGTTTCGTAAGAATAATGTAATTTCAATADSMKC 221
 OY 40 ----ArgIlePheLeuProThrIleTyrPheIleIlePheLeuThrGlyIleVal----- 56
 |||||
 DB 222 RNNANNAATCTTCCTCGCCACCATCTACTCATCATCTTTCTTAAGTGCATTTGCTKTYST 281
 OY 57 --GlyAsnGlyLeuValIleLeuValMetGlyTyrGlnLysLysLeuArg----- 72
 |||||
 DB 282 GVGCGAATGATGGTGCATCTCGTACGAGGTTACAGAGAATACTGAGAGNGVNGY 341
 OY 73 --SerMetThrAspLysTyrArgLeuHisLeuSerValAlaAspLeuPheVal----- 90
 |||||
 DB 342 KKRSCATGACGAGACAGTACAGGCTGACCTGTCAGTGGCCGACCTCTCTTGM-TDKY 400
 OY 91 -----IleThrLeuProPheTrpAlaValAspAlaMetAlaAspTrpTyrPhe----- 106
 |||||
 DB 401 RHSVADTCATCAGCTTCCTTCGSCAGTTGATGCGCGTGGCAACATGCTTTTVA 460
 OY 107 -----GlyLysPheLeuCysLysAlaValHisIleIleTyrThrValAsnLeu---- 122
 |||||
 DB 461 VDAVAMWGGACACTCTATGCAAGGAGTGCATGTCATCATCACTGACCTGAGN 520
 OY 123 -----TyrSerSerValLeuIleLeuAlaPheIleSerLeuAspArgTyrLeuAla 139
 |||||
 DB 521 CKAHVHTVNTCAGAGTGTCTCATCTGCGCTTCATCAGCTGAGCGCTACTGCGC 580
 OY 140 -----IleValHisAlaThrAsnSerGlnArgProArgLysLeuLeuAlaGluLys 156
 |||||
 DB 581 ASSVASDRYATGCTCAGCAGCACCAAGTCAGAGGCCAAGAGAGCTTTGGCTAANAAG 640
 OY 157 Ala-----ValTyrValGlyValTrpIleProAlaLeuLeuThrIle-Pr 172
 |||||
 DB 641 VH-ATNSHRKAKGTGTCTATGTTGGCTGTGATCCCTGCTCTGCTACTATTC 699
 OY 172 o-----AspPheIlePheAlaAspAlaSerGlnLysPheSerGlnGlyAspAs 189
 |||||
 DB 700 GAVVYGVWATDCTTCATCTTGGCCACGTC-----AGTGAGGCGAGATGA 744
 OY 189 PARGTyrIleCysAspArg-----LeuTyrProAspSerLeuTrpMetValVa 205
 |||||
 DB 745 CAGATATCTGTGTAGCA-NVSADRYDGGTCTGACCCCAATGACTGTGGGTGTGT 803
 OY 205 lPheGlnPheGlnHisIle-----MetValGlyLeuIleLeuProGlyIleValI 222
 |||||
 DB 804 GTTCACAGTTTACGACATCRYNDWVVAHTGGTTGGCTTATCTGCTGATTTGTAT 863
 OY 222 eleuSerCysTyrCysIle-----IleIleSerLysLeuSerHisSerLysGlyH 239
 |||||
 DB 864 CCTGCTCTGCTATGTCATMGVGVSCYATATCATCTCCAAAGTGTCACTCCAAAGGCCA 923
 OY 239 sGlnLysArgLysAla-----LeuLysThrThrValIleLeuIleLeuAlaPh 255
 |||||
 DB 924 CCAGAGAGCGCAAGGCCCKSHSKGKRATCAAGACCACTGATCTCATCTCGCTTT 983
 OY 255 ePheAlaCysTrpLeuPro-----TyrTyrValGlyIleSerIleAspSerPheIle 272
 |||||
 DB 984 CTTCGCCCTGTGGCTCTKTVAACWPTACATTTGGATGAGCATGACATCTTCATC 1043
 OY 273 leuLeuGlyValIleLys-----GlnGlyCysAspPheGluSerIleValHisLysTr 290
 |||||
 DB 1044 CTCCTGAAATCATCAAAVYGSDSKGCAGAGGTGTGAGTTGAGAACACTGTGCACAAAGTG 1103

OY 290 pIleSerIleThr-----Glu-AlaLeuAlaPhePheHisCysCysLeuAsnProI 307
 |||||
 DB 1104 GATTTCCATTCACCGGCNTVHKWSTAGGCCCTTCTTCTTCTGACTGTGTGAACCCCA 1163
 OY 307 leIeuTyrAlaPhe-----LeuGlyAlaLysPheLysSerSerAlaGlnHisAlaL 324
 |||||
 DB 1164 TCCCTCTATGC-TTTCAAHCNVACTTGTGAGCCAAATTTAAACCTGCCCCAGCAGCAGC 1222
 OY 324 euAsnSerMet-----SerArgLysSerSerLeuLysIleLeuSerLysGly 339
 |||||
 DB 1223 TCACCTCTGTGAGCAKKTSAHATSVSCAGAGGTCACCTCAAGATCTCTCCAAAGGA 1282
 OY 340 LysArgGlyGlyHis-----SerSerValSerThrGluSerGluSerSerSe 355
 |||||
 DB 1283 AAGCAGAGTGACACATTTRESSSKSKRGSHCATCTGTTCCACTAGTGTGACTTCAAG 1342
 OY 355 rPheHisSerSer 359
 |||||
 DB 1343 TTTTCACCTCCAGC 1355

RESULT 7

US-09-796-692-2611

; Sequence 2611, Application US/09796692

; Publication No. US20020198362A1

GENERAL INFORMATION:

; APPLICANT: Gaiger, Alexander

; APPLICANT: Algate, Paul A.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THER

; FILE REFERENCE: 2077.001200

; CURRENT APPLICATION NUMBER: US/097966,692

; PRIOR FILING DATE: 2001-03-01

; PRIOR APPLICATION NUMBER: 60/186,126

; PRIOR FILING DATE: 2000-03-01

; PRIOR APPLICATION NUMBER: 60/190,479

; PRIOR FILING DATE: 2000-03-17

; PRIOR APPLICATION NUMBER: 60/200,545

; PRIOR FILING DATE: 2000-04-27

; PRIOR APPLICATION NUMBER: 60/200,303

; PRIOR FILING DATE: 2000-04-28

; PRIOR APPLICATION NUMBER: 60/200,779

; PRIOR FILING DATE: 2000-04-28

; PRIOR APPLICATION NUMBER: 60/200,999

; PRIOR FILING DATE: 2000-05-01

; PRIOR APPLICATION NUMBER: 60/202,084

; PRIOR FILING DATE: 2000-05-04

; PRIOR APPLICATION NUMBER: 60/206,201

; PRIOR FILING DATE: 2000-05-22

; PRIOR APPLICATION NUMBER: 60/218,950

; PRIOR FILING DATE: 2000-07-14

; PRIOR APPLICATION NUMBER: 60/222,903

; PRIOR FILING DATE: 2000-08-03

; PRIOR APPLICATION NUMBER: 60/223,416

; PRIOR FILING DATE: 2000-08-04

; PRIOR APPLICATION NUMBER: 60/223,378

; PRIOR FILING DATE: 2000-08-07

; NUMBER OF SEQ ID NOS: 9597

; SOFTWARE: FASTSEQ for Windows Version 3.0

; SEQ ID NO 2611

; LENGTH: 421

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-796-692-2611

Alignment Scores:

Pred. No.: 3,91e-66 Length: 421

Score: 657.50 Matches: 125

Percent Similarity: 92.36% Conservative: 8

Best Local Similarity: 86.81% Mismatches: 6

Query Match: 35.22% Indels: 5

DB: 9 Gaps: 1

ORGANISM: Homo sapiens
US-10-251-385-19

Alignment Scores:
Pred. No.: 4,65e-57 Length: 1107
Score: 584.00 Matches: 124
Percent Similarity: 54.26% Conservative: 67
Best Local Similarity: 35.23% Mismatches: 139
Query Match: 31.28% Indels: 22
DB: 9 Gaps: 5

US-09-367-052-2 (1-359) x US-10-251-385-19 (1-1107)

```

OY 12 AspaNtYrSerGluGluValAlGlySerGlyAspTyrAspSerAsn-----Lys 27
DB 61 GAGAACTTACAGTCTTCTTATGACTATGAGAAAAGAGATGACTGCTGTACCTCC 120
OY 28 GluProCysPheArgAspGluAsnValHisPheAsnArgIlePheLeuProThrlIleTyr 47
DB 121 CCGCCCTCCACAGAGACTTCAGCTGAACCTGCAGCGGCTTCCTCCAGCCCTTAC 180
OY 48 PheIleIlePheLeuThGlyIleValAlGlySngIleValIleLeuValMetClyTyr 67
DB 181 AGCCCTCTTCTTCTGCTGCGCTGCGCAAGCGGCGGCGAGCCGCTGCTGAGC 240
OY 68 GluLysLysLeuArgSerMetThrAspLysTyrArgLeuHisLeuSerValAlAspLeu 87
DB 241 CCGCGGACAGCCCTGAGCAGCAGCAGCAGCTTCTGCTCCACCTGAGCTGAGCAGCAGC 300
OY 88 LeuPheValIleThrLeuProPheThrAlaValAlAspAlaMetAlaAspTrpTyrPheCly 107
DB 301 CTGCTGCTGCTGACACTGCGCTGCGCAGTGCAGCTGCGCTGAGTGGCTCTTGGC 360
OY 108 LysPheLeuCysLysAlaValHisIleIleTyrThrValAsnLeuTyrSerSerValLeu 127
DB 361 TCTGCTCTCTGCAAGTGGCAGCTGCGCTTCAACATCACTTCTGAGCAGGAGCCCTC 420
OY 128 IleLeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThrAsnSerGln 147
DB 421 CTGCTGCGCTGATGATGACTTTCAGCCGTAACCTGACATAGTTCAGCCAGCAGCTTAC 480
OY 148 ArgProArgLysLeuLeuAlaGluLysAlaValTyrValAlGlyValTrrIleProAlaLeu 167
DB 481 CCGCGGCGGCGCGCGCGCGCTGACCTGACCTGCTGCTGCTGCGGCTGCTGCTGCTG 540
OY 168 LeuLeuThrIleProAspPheIlePheAlaAspValSerGlnGlyAspIleSerGlnGly 187
DB 541 CTGTTGCGCTCCAGACTTCACTTCTGCTG-----GCCACACAC 582
OY 188 AspAspArgTyr-----IleCysAspArgLeuTyrProAspSerLeuTrpMetVal 204
DB 583 GACGAGCGGCTCAAGCCGACGACGACGACGACGACGACGACGACGACGACGACGACG 639
OY 205 ValPheGlnPheGlnHisIleMetValGlyLeuIleLeuProGlyIleValIleLeuSer 224
DB 640 GCTCTGCGGCTGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 699
OY 225 CysTyrCysIleIleIleSerLysLeuSerHisSerLysGlyHisGlnLysArgLysAla 244
DB 700 TGTATGCGCCACATCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 759
OY 245 LeuLysThrThrValIleLeuIleLeuAlaPhePheAlaCysTrpLeuProTyrTyrVal 264
DB 760 ATGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 819
OY 265 GlyIleSerIleAspSerPheIleLeuLeuGlyValIleLysGlnGlyCysAspPheGlu 284
DB 820 GTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 879
OY 285 SerIleValHisLysTrpIleSerIleThrGlnAlaLeuAlaPheHisLysCysGln 304
DB 880 AGCAGGTAAGACGTGGCAAGTCGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 939

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OY 305 AsnProIleLeuTyrAlaPheLeuGlyAlaLysPheLysSerSerAlaGlnHisAlaLeu 324
DB 940 AACCCCTGCTTATGCTTGTATGAGGGGTCAAGTCCGAGGAGGATGATGATGCTGCTC 999
OY 325 AsnSerMetSerArgGlySerSerLeuLysIleLeuSerLysGlyLysArgGlyGlnHis 344
DB 1000 -----TTCGGCTGGGCTGCCCCCAACAGAGAGGGCTCCAG 1035
OY 345 SerSerValSerThrGluSerGluSerSerPhe 356
DB 1036 AGCAGCCATCGTCTTCCCGCGGAGTTCACTCTGG 1071

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RESULT 10

US-10-225-567A-73
Sequence 73, Application US/10225567A
Publication No. US20030113798A1

GENERAL INFORMATION:

APPLICANT: Lifespan Biosciences

APPLICANT: Brown, Joseph P.

APPLICANT: Burmer, Glenna C.

APPLICANT: Roush, Christine L.

TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPT

FILE REFERENCE: 1920-4-4

CURRENT FILING DATE: US/10/225, 567A

PRIOR APPLICATION NUMBER: 2001-12-19

PRIOR FILING DATE: 2000-12-19

NUMBER OF SEQ ID NOS: 2292

SOFTWARE: PatentIn version 3.1

SEQ ID NO 73

LENGTH: 1670

TYPE: DNA

ORGANISM: Homo sapiens

US-10-225-567A-73

Alignment Scores:
Pred. No.: 8.82e-57 Length: 1670
Score: 584.00 Matches: 124
Percent Similarity: 54.26% Conservative: 67
Best Local Similarity: 35.23% Mismatches: 139
Query Match: 31.28% Indels: 22
DB: 9 Gaps: 5

US-09-367-052-2 (1-359) x US-10-225-567A-73 (1-1670)

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OY 12 AspaNtYrSerGluGluValAlGlySerGlyAspTyrAspSerAsn-----Lys 27
DB 129 GAGAACTTACAGTCTTCTTATGACTATGAGAAAAGAGATGACTGCTGTACCTCC 188
OY 28 GluProCysPheArgAspGluAsnValHisPheAsnArgIlePheLeuProThrlIleTyr 47
DB 189 CCGCCCTGCCACAGAGACTTCAGCTGAACCTGCAGCGGCTTCCTCCAGCCCTTAC 248
OY 48 PheIleIlePheLeuThGlyIleValAlGlySngIleValIleLeuValMetClyTyr 67
DB 249 ACCCTCTCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 308
OY 68 GluLysLysLeuArgSerMetThrAspLysTyrArgLeuHisLeuSerValAlAspLeu 87
DB 309 CCGCGGACAGCCCTGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 368
OY 88 LeuPheValIleThrLeuProPheThrAlaValAlAspAlaMetAlaAspTrpTyrPheCly 107
DB 369 CTGCTGCTGCTGACACTGCGCTGCGCAGTGCAGCTGCGCTGCTGCTGCTGCTGCTG 428
OY 108 LysPheLeuCysLysAlaValHisIleIleTyrThrValAsnLeuTyrSerSerValLeu 127
DB 429 TCTGCTCTTCTGCAAGTGGCAGCTGCTTCAACATCACTTCTGAGCAGGAGCCCTC 488
OY 128 IleLeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThrAsnSerGln 147
DB 489 CTGCTGCTGCTGATGACTTTCAGCCGCTTACGACATAGTTCATGACCCAGCTTAC 548

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Db 1068 -----TTGGGCTGGGCTGCCCAACAGAGAGGGCTCCAG 1103
Oy 345 SerSerValSerThrGluSerGluSerSerPhe 356
Db 1104 AGGAGCCATGCTCTCCCGCGGATTCATCTGG 1139

RESULT 12
US-10-251-385-173
Sequence 173, Application US/10251385
Publication No. US20030105292A1
GENERAL INFORMATION:
APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: No. US20030105292A1-Endogenous, Constitutively Activated Human G
TITLE OF INVENTION: Protein-Coupled
TITLE OF INVENTION: Receptors
FILE REFERENCE: AREN-0040
CURRENT APPLICATION NUMBER: US/10/251,385
PRIOR APPLICATION NUMBER: US/09/170,496
PRIOR FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 294
SOFTWARE: PatentIn version 3.1
SEQ ID NO 173
LENGTH: 1107
TYPE: DNA
ORGANISM: Homo sapiens
US-10-251-385-173

Alignment Scores:
Pred. No.: 1,34e-56 Length: 1107
Score: 580.00 Matches: 124
Percent Similarity: 53.98% Conservative: 66
Best Local Similarity: 35.23% Mismatches: 140
Query Match: 31.07% Indels: 22
Gaps: 5
Db: 9

US-09-367-052-2 (1-359) x US-10-251-385-173 (1-1107)

Oy 12 AspaSerValSerThrGluValGlySerGlyAspTyrAspSerAsn-----Lys 27
Db 61 GAGAACTTCACTCTTCTATGATGAGAAAACGAGAGTCTGCTGATACCTCC 120
Oy 28 GluProCysPheArgAspGluAsnValHisPheAsnArgIlePheLeuProThrIleTyr 47
Db 121 CGGCCCTGCTCCACAGAGACTTCAAGCTTGAACCTTCCGCTGCTGCGACCCCTTAC 180
Oy 48 PheIleIlePheLeuThrGlyIleValGlyAsnGlyLeuValIleLeuValMetClyTyr 67
Db 181 AGCCTCCTCTTTCGCTGGGCTGCTGCGCAACGGCGGCGGAGCGGCTGCTGAGC 240
Oy 68 GlnLysLysLeuArgSerMetThrAspLysTyrArgLeuHisLeuSerValAlaAspLeu 87
Db 241 CGCGGAGACGCTGAGCAGCAGCAGCAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
Oy 88 LeuPheValIleThrLeuProPheThrAlaValAspIleMetAlaAspTyrTyrPheGly 107
Db 301 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
Oy 108 LysPheLeuCysLysAlaValHisIleIleTyrThrValAsnLeuTyrSerSerValLeu 127
Db 361 TCTGCGCTCTCAAGAGTGGCAGTGGCTCTTCAACATCACTTCTAGCAGAGACCTTC 420
Oy 128 IleLeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThrAsnSerGln 147
Db 421 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
Oy 148 ArgProArgLysLeuLeuAlaGluLysAlaValIleValIleGlyValIleTyrIleProAlaLeu 167
Db 481 CGCGGAGGCGCGCGCGCGCGCTGACCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTG 540
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Oy 168 LeuLeuThrIleProAspPheIlePheAlaAspValSerGlnGlyAspIleSerGlnGly 187
Db 541 CTTTCCGCCCTCCACAGACTTATCTTCTGCG-----GCCACAC 582
Oy 188 AspaSerValTyr-----IleCysAspArgLeuTyrProAspSerLeuTyrMetVal 204
Db 583 GACGAGGCGCTCAAGCGCACCCACTGCCAATCACTTCCA---CAGGTGGCGCCGACG 639
Oy 205 ValPheGlnPheGlnHisIleMetValGlyLeuIleLeuProGlyIleValIleLeuSer 224
Db 640 GCTCTGCGGCTGCTGCAAGCTGCTGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTTAC 699
Oy 225 CysTyrCysIleIleIleSerLysLeuSerHisSerLysGlnHisGlnLysArgLysAla 244
Db 700 TGTATGCTCCACATCCAGCGCGCTGCTGCTGCTTCCAGAGGCGCACCGCGCTGCGCGCC 759
Oy 245 LeuLysThrThrValIleLeuIleLeuAlaPheAlaCysTyrLeuProTyrTyrVal 264
Db 760 AAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 819
Oy 265 GlyIleSerIleAspSerPheIleLeuLeuGlyValIleLysGlnGlyCysAspPheGlu 284
Db 820 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 879
Oy 285 SerIleValHisLysTyrPheSerIleThrGluAlaLeuAlaPheHisCysCysLeu 304
Db 880 AGCAGGGTAGACGTCGGCAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 939
Oy 305 AsnProIleLeuTyrAlaPheLeuGlyAlaLysPheLysSerSerAlaGlnHisAlaLeu 324
Db 940 AACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 999
Oy 325 AsnSerMetSerArgLysSerSerLeuLysIleLeuSerLysGlyLysArgGlyHis 344
Db 1000 -----TTGCGCTGGCTGCCCGCAACAGAGAGGGCTCCAG 1035
Oy 345 SerSerValSerThrGluSerGluSerSerPhe 356
Db 1036 AGGAGCCATGCTCTCCCGCGGATTCATCTGG 1071

RESULT 13
US-10-106-698-2125
Sequence 2125, Application US/10106698
Publication No. US20030109690A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypept
FILE REFERENCE: PA005P1
CURRENT APPLICATION NUMBER: US/10/106,698
PRIOR FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: PCT/US00/26524
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US 60/157,137
PRIOR FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: US 60/163,280
PRIOR FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 8564
SOFTWARE: PatentIn Ver. 3.0
SEQ ID NO 2125
LENGTH: 1877
TYPE: DNA
ORGANISM: Homo sapiens
US-10-106-698-2125

Alignment Scores:
Pred. No.: 1.14e-55 Length: 1877
Score: 575.00 Matches: 123
Percent Similarity: 53.69% Conservative: 66
Best Local Similarity: 34.94% Mismatches: 141
Query Match: 30.80% Indels: 22
Gaps: 5
Db: 9

US-09-367-052-2 (1-359) x US-10-106-698-2125 (1-1877)
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QY 12 AspaNtyrSerGluValGlySerGlyAspTyrAspSer-----AsnLys 27
Db 374 GAGAACTTACAGCTCTTCTTACTATGAGAGAAAAAGAGATGAMTCTGCTGATACGCC 433
QY 28 GluProCysPheIleAspGluAsnValHisPheAsnArgIlePheLeuProThrIleTyr 47
Db 434 CCGGCTCTCCACAGAGACTTCAAGCTTGAACCTTCCAGCGGCTCTTCCAGCCCTTCMAC 493
QY 48 PheIleIlePheLeuThrGlyIleValGlyAsnGlyLeuValIleLeuValMetGlyTyr 67
Db 494 AGCTCTCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 553
QY 68 GluLysLysLeuArgSerMetThrAspLysTyrArgHisLysLeuSerValAlaAspLeu 87
Db 554 CGGGGAGACGCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 613
QY 88 LeuPheValIleThrLeuProPheThrAlaValAlaAspAlaMetAlaAspTyrPheGly 107
Db 614 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 673
QY 108 LysPheLeuCysLysAlaValHisIleIleTyrThrValAsnLeuTyrSerValLeu 127
Db 674 TCTGAGCTCTGCAAGTGGCAGTGGCTCTTCAACATCACTTCTACGAGAGAGAGAGAG 733
QY 128 IleLeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThrAsnSerGln 147
Db 734 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 793
QY 148 ArgProArgLysLeuLeuAlaGlyLysAlaValTyrValGlyValTyrIleProAlaLeu 167
Db 794 CGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 853
QY 168 LeuLeuThrIleProAspPheIlePheAlaAspValSerGlnGlyAspIleSerGlnGly 187
Db 854 CTTTTCGGCTTCCAGAGACTTATCTTCTGCTG-----GCCACACAC 895
QY 188 AspaAspArgTyr-----IleCysAspArgLeuTyrProAspSerLeuTyrMetVal 204
Db 896 GACGAGGCGCTCAAGCCAGCCAGCTGCAATCAACTGCCA---CAGGTGGGGCGGACG 952
QY 205 ValPheGlnPheGlnHisIleMetValGlyLeuLeuLeuProGlyIleValIleLeuSer 224
Db 953 GCTCTGCGGCTGCTGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1012
QY 225 CysTyrCysIleIleIleSerLysLeuSerHisSerLysGlnHisGlnLysArgLysAla 244
Db 1013 TGTATGCCCCACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1072
QY 245 LeuLysThrThrValIleLeuIleLeuAlaPhePheAlaCysTyrLeuProTyrTyrVal 264
Db 1073 ATGGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1132
QY 265 GlyIleSerIleAspSerPheIleLeuLeuGlyValIleLysGlnGlyCysAspPheGlu 284
Db 1133 GTGGTGGCTGCTGCAATCTGATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1192
QY 285 SerIleValHisLysTyrPheIleSerIleThrGluAlaLeuAlaPhePheHisCysLysLeu 304
Db 1193 AGCAGGAGTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1252
QY 305 AsnProIleLeuTyrAlaPheLeuGlyAlaLysPheLysSerSerAlaGlnHisAlaLeu 324
Db 1253 AACCCTGCTCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1312
QY 325 AsnSerMetSerArgGlySerSerLeuLysIleLeuSerLysGlyLysArgGlyLysHis 344
Db 1313 -----TTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1348
QY 345 SerSerValSerThrGluSerGluSerSerPhe 356
Db 1349 AGGAGCAGCATGCTTCCCGCGGAGATTCATCTGG 1384

```

```

RESULT 14
US-10-120-394-19
; Sequence 19, Application US/10120394
; Patent No. US20020160015A1
; GENERAL INFORMATION:
; APPLICANT: Wells, Timothy N.C.
; Power, Christine A.
; TITLE OF INVENTION: CHEMOKINE RECEPTOR ABLE TO BIND TO MCP-1, MIP-1 ALPHA AND/OR RANTES AND ITS USES
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESS: NIXON & VANDERHAYE P.C.
; STREET: 1100 NO. US20020160015A1th Glebe Rd. 8th floor
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US 09/614,256
; FILING DATE: 12-JUL-2000
; APPLICATION NUMBER: US 08/875,573
; FILING DATE: 31-OCT-1997
; APPLICATION NUMBER: PCT/GB96/00143
; FILING DATE: 24-JAN-1996
; APPLICATION NUMBER: GB 9501683.8
; FILING DATE: 27-JAN-1995
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1607 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 183..1262
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-10-120-394-19

Alignment Scores:
Score: 2,93e-55 Length: 1607
Pred. No.: 570.50 Matches: 120
Percent Similarity: 57.01% Conservative: 63
Best Local Similarity: 37.38% Mismatches: 125
Query Match: 30.56% Indels: 13
DB: 9 Gaps: 6

US-09-367-052-2 (1-359) x US-10-120-394-19 (1-1607)
QY 1 MetGluProIleSerValSerIleTyrThrSerAspaNtyrSerGluValGlySer 20
Db 183 ATGAACCCACAGATATAGCAGATACCACTCGAT-----GAAAGCATATACAG 233
QY 21 GlyAsp-----TyrAspSerAsnLysGluProCysPheArgAspGluAsnValHisPhe 38
Db 234 AATTACTATCTGTATGAAGATATCCCAAGCTTGCACCAAGAAGAGCATCAAGCATTT 293
QY 39 AsnArgIlePheLeuProThrIleTyrPheIleIlePheLeuThrGlyIleValGlyAsn 58
Db 294 GGGAGGCTCTTCCGCCCCCACTGATATCTGTTTGTATTTGGTCTGCTGGAAT 353
QY 59 GlyLeuValIleLeuValMetGlyTyrGlnLysLysLeuArgSerMetThrAspLysTyr 78
Db 354 TCTGTGGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 413

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Qy 79 ArgLeuHisLeuSerValAlaAspLeuPheValIleThrLeuProPheIleVal 98
Db 414 CTGCTCAACCTGGCAGCTGCGATCTGCTCTGCTTTTCCCTTTTGGGGCTAC 473
Qy 99 AspaIaMetAlaAspTyrPheGlyLysPheLeuCysLysAlaValHisIleIleTyr 118
Db 474 TATCAGACAGACCGAGTGGTGGCTAGCTGTCAGAGATGATTTCTCGATGATGAC 533
Qy 119 ThrValAsnLeuTyrSerSerValLeuIleLeuAlaPheIleSerLeuAspArgTyrLeu 138
Db 534 TTGCTGGGCTTTTACAGGCGATATCTTTGCTCATGCTCATGACATGATGATGATG 593
Qy 139 AlaIleValHisAlaThrAsnSerGlnArgProArgLysLeuAlaGluLysAlaVal 158
Db 594 GCGATAGTGCACGCGGGTGTTCCTTGAGGCGCAGAGACCTGACTTATGGGCTCATCACC 653
Qy 159 TyrValGlyValTrrPlePheAlaLeuLeuLeuThrIleProAspPheIlePheAlaAsp 178
Db 654 AGTTGGCTACATGCTGAGTGGCTGTGTGCGCTCCCTTCCTGGCTTTCGTCAGGACT 713
Qy 179 ValSerGlnLysPheIleSerGlnGlyAspAspArgTyrIleCysAspArgLeuTyrPro 198
Db 714 TGT-----TATACTGAGCGCAGACCATACCTAC--TGCAGAAACCAAGTACTCT 758
Qy 199 -----AspSerLeuTrrPmetValValPheGlnPheGlnHisIleMetValGlyLeuIle 216
Db 759 CTCAGCTCCAGCAGCTGGAAGCTTCTCAGCTCCCTCGAATCATCATCTCGATGTTGGTG 818
Qy 217 LeuProGlyIleValIleLeuSerCysTyrCysIleIleIleSerLysLeuSerHisSer 236
Db 819 ATCCCTTAGGAGCATGCTGTTTGGTATCATCATGATCATGATCAGACCTTGACCATTTGT 878
Qy 237 LysGlyHisGlnLysArgLysAlaLeuLysThrThrValIleLeuIleLeuAlaPhePhe 256
Db 879 AAAAATGAGAGAGAACAGACGCGGTGAGATGATCTTGGCGGTGGTCTCTCTCTT 938
Qy 257 AlaCysTrrPleuProTyrTyrValGlyIleSerIleAspSerPheIleLeuLeuGlyVal 276
Db 939 GGGTCTGACACCTTACACATAGTCTCTTCCAGAGACCTCGTGACCTGAGATGTC 998
Qy 277 IleLysGlnGlyCysAspPheGluSerIleValHisLysTrrPleSerIleThrGluAla 296
Db 999 CTT---CAGGACTCCACCTTGAAGATACCTTGCACTATGCCATCCAGCGCAGAAACT 1055
Qy 297 LeuAlaPhePheHisCysCysLeuAsnProIleLeuTyrAlaPheLeuGlyAlaLysPhe 316
Db 1056 CTGGCTTTTGTTCACCTGCTGCTTAAATCCATCTTCTTTTCTGGGGAGAAATTT 1115
Db 317 Lys 317
Db 1116 CGC 1118

RESULT 15
-US-09-764-413-19
Sequence 19, Application US/09764413
Publication No. US20020187930A1

GENERAL INFORMATION:
APPLICANT: Wells, Timothy N.C.
Power, Christine A.
TITLE OF INVENTION: A CHEMOKINE RECEPTOR ABLE TO BIND TO
MCP-1, MIP-1 ALPHA AND/OR RANTES. ITS USES
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHIVE P.C.
STREET: 1100 NO. US20020187930A1th Giebe Rd. 8th floor
CITY: Arlington
STATE: VA
COUNTRY: USA
ZIP: 22201-4741
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/764,413
FILING DATE: 19-Jan-2001
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/875,573
FILING DATE: <unknown>
APPLICATION NUMBER: GB 9501683.8
FILING DATE: 27-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Wilson, Mary J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 1430-172
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
TELEFAX: 703-816-4100
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 1607 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 183..1262
SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-764-413-19
Alignment Scores:
Pred. No.: 2,93e-55 Length: 1607
Score: 570.50 Matches: 120
Percent Similarity: 57.01% Conservative: 63
Best Local Similarity: 37.38% Mismatches: 125
Query Match: 30.56% Indels: 13
Gaps: 6
US-09-367-052-2 (1-359) x US-09-764-413-19 (1-1607)
Qy 1 MetLupProIleSerValSerIleTyrThrSerAspAsnTyrSerGluGluValGlySer 20
Db 183 ATGACACCCAGCAGATATGACGATACACACCTCGAT-----GAACCATATATACAGC 233
Qy 21 GlyAsp-----TyrAspSerAsnLysGluProCysPheArgAspGluAsnValHisPhe 38
Db 234 AATTACTATGCTGTATGAAGATATCCCAAGCTTGACCAAGAGAGCATCAAGCATTT 293
Qy 39 AsnArgIlePheLeuProThrIleTyrPheIleIlePheLeuThrGlyIleValGlyAsn 58
Db 294 GGGAGCTCTTCTGCCCCCAGCTGATATCTTGTGTTTGTATTTGGCTGCTGGAAT 353
Qy 59 GlyLeuValIleLeuValMetGlyTyrGlnLysLysLeuArgSerMetHisAspLysTyr 78
Db 354 TCTGTGTGGTTCGTCGCTCTTCAATATACAGCGCTGACCTGCATGACATGATGATG 413
Qy 79 ArgLeuHisLeuSerValAlaAspLeuPheValIleThrLeuProPheIleVal 98
Db 414 CTGCTCAACCTGGCAGCTGCGATCTGCTCTGCTTTTCCCTTTTGGGGCTAC 473
Qy 99 AspaIaMetAlaAspTyrPheGlyLysPheLeuCysLysAlaValHisIleIleTyr 118
Db 474 TATCAGACAGACCGAGTGGTGGCTAGCTGTCAGAGATGATTTCTCGATGATGAC 533
Qy 119 ThrValAsnLeuTyrSerSerValLeuIleLeuAlaPheIleSerLeuAspArgTyrLeu 138
Db 534 TTGCTGGGCTTTTACAGGCGATATCTTTGCTCATGCTCATGACATGATGATGATG 593
Qy 139 AlaIleValHisAlaThrAsnSerGlnArgProArgLysLeuAlaGluLysAlaVal 158
Db 594 GCGATAGTGCACGCGGGTGTTCCTTGAGGCGCAGAGACCTGACTTATGGGCTCATCACC 653

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: July 12, 2003, 16:49:14 ; Search time 1186 Seconds

(without alignments)
4902.344 Million cell updates/sec

Title: US-09-367-052-2

Perfect score: 1867

Sequence: 1 MEPISVSIYTSNDYSEEYGS.....KRGHSVSTSESSSFHSS 359

Scoring table:

BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Switched: 16154066 segs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n model -DEV=x1h
-QO/cgn2.1/USPTO.spool/US09367052/runat_10072003.100045.10395/app.query.fasta.1.519
-DB=EST -QFMT=fastlap -SUFIX=1st -MINMATCH=0.1 -DOOPCL=0 -DOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blomsu62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=Pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09367052.ecgn.1.1.1456 -runat_10072003.100045.10395 -NCPU=6 -ICPU=3
-NO MAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPLOCK=100 -LONGLOS
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FEAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estlin:*
4: em_estlmv:*
5: em_estlov:*
6: em_estlpl:*
7: em_estro:*
8: em_hlc:*
9: gb_estcl:*
10: gb_estcl2:*
11: gb_hlc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estlum:*
16: em_estlum:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_lun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1422.5	76.2	1051	13	BM545259
2	1238.5	66.3	910	13	BM162229
3	1196	64.1	950	14	BM176167
4	1188	63.6	891	13	BM182463
5	1179	63.1	1034	14	BM920800
6	1122	60.1	827	13	BM176166
7	1098	58.8	913	13	BM051973
8	1096.5	58.7	875	13	BM175617
9	1093.5	58.2	905	13	BM175409
10	1086.5	58.0	765	13	BM387369
11	1082.5	55.0	750	12	BM613352
12	1027.5	55.0	745	13	BM191701
13	987.5	52.9	782	12	BM685801
14	986	52.8	846	12	BM338608
15	979.5	52.5	742	13	BM159787
16	979	52.4	958	12	BM174412
17	975.5	52.2	702	13	BM176118
18	974.5	52.2	582	12	BM145042
19	973.5	52.1	680	14	BM109515
20	971.5	52.0	853	9	AJ454503
21	967.5	51.8	728	9	AU117058
22	958	51.3	955	12	BM173867
23	942	50.5	753	13	BM915636
24	934.5	50.1	952	13	BM182169
25	924.5	49.5	703	13	BM176576
26	923	49.4	553	12	BM145062
27	917.5	49.1	676	9	AJ398841
28	910.5	48.8	658	13	BM183125
29	907.5	48.6	793	9	AA182270
30	904	48.4	528	12	BM277031
31	897	48.0	858	12	BM797340
32	893.5	47.0	858	9	AJ452057
33	890.5	47.7	775	9	AJ446828
34	881	47.2	585	10	BM627479
35	877.5	47.0	894	13	BM177103
36	876	46.9	639	9	AA816049
37	865	46.3	748	13	BM546899
38	853	45.7	628	10	BM227957
39	850.5	45.6	755	9	AJ452672
40	849	45.5	890	13	BM181979
41	848.5	45.4	757	9	AJ454629
42	848	45.4	612	12	BM488397
43	843	45.2	645	9	AI884548
44	839.5	45.0	741	9	AJ447649
45	836.5	44.8	671	13	BM059654

ALIGNMENTS

RESULT 1	BM545259	1051 bp	mrna	linear	EST 20-FEB-2002
LOCUS	BM545259				
DEFINITION	AGENCOURT 6497171	NIH_MGC_124	Homo sapiens	CDNA clone IMAGE:5726963	
ACCESSION	BM545259				
VERSION	BM545259.1	GI:18777197			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 1051)				
AUTHORS	NIH-MGC	http://mgi.nci.nih.gov/			
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)				

JOURNAL
COMMENT

Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-riemail.nih.gov
Tissue Procurement: Invitrogen
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: LLM12/20 row: e column: 12
High quality sequence start: 20
High quality sequence stop: 753.
Location/Qualifiers

FEATURES
source

1. 1051
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5726963"
/clone_lib="NIH_MGC_116"
/tissue_type="hippocampus"
/lab_host="DH10B"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: EcoRV (destroyed); Site_2: NotI; RNA source male hippocampus, age 27. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 0.9-4 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 012."
BASE COUNT 240 a 302 c 238 g 271 t
ORIGIN

Alignment Scores:

Pred. No.: 5,22e-165 Length: 1051
Score: 1422.50 Matches: 281
Percent Similarity: 91.598 Conservatave: 24
Best Local Similarity: 84.388 Mismatches: 18
Query Match: 76.198 Indels: 10
DB: 13 Gaps: 1

US-09-367-052-2 (1-359) x BM545259 (1-1051)

QY 6 ValSerIleYrThSerAspAsnTySerGluGluValGlySerGlyAspTyRAspSer 25
DB 77 ATCACTAATATACACTTCAAGATTAACACACGAGAAATAGGCTCAGGGAGACTATGACTCC 136
QY 26 AsnLysGluProCysPheArgAspLysValHisPheAsnArgIlePheLeuProthr 45
DB 137 ATGAAGGAACCTGTTCCGTGAAATAATATTTCATAATTAATCTTCCTGCCACAC 196
QY 46 IleYrPheIleIlePheLeuThrGlyIleValGlyAsnGlyLeuValIleLeuValMet 65
DB 197 ATCTACTCCATCATCTTTTAACCTGCGCATGTGGSCAATGATGTGTATCTCTGTCATG 256
QY 66 GlyTyGlnLysLysLeuArgSerMetThrAspLysTyArgLeuHisLeuSerValAla 85
DB 257 GGTTCACGAGAACTGAGAGCATGACGAGCAGTAGACGCTGCACCTGTCATGGCC 316
QY 86 AspLeuPheValIleThrLeuProPheTrpAlaValAspAlaMetAlaAspTrpYr 105
DB 317 GACCCCTCTTGTTCATACGCTTCCCTTGGGAGTTGATGGCCGTGAGCAACCTGGTAC 376
QY 106 PheGlyLysPheLeuCysLysAlaValHisIleIleYrThValAsnLeuTySerSer 125
DB 377 TTTGGGAACCTCTTATGCAAGGACATGTCATCTACACAGTAACTCTACGCGAGT 436
QY 126 ValLeuIleLeuAlaPheIleSerLeuAspArgTyRLeuAlaIleValHisAlaThrAsn 145
DB 437 GTCTCATCTCTGGCTTCATAGCTGACGCGCTACCTGCACATGTCACAGCCACCAAC 496
QY 146 SerGlnArgProArgLysLeuLeuAlaGluLysAlaValTyRValGlyValTrpIlePro 165
DB 497 AGTCAGAGGCCAAGAACCTGTGGCTGAAAAGGTGTCTATGTGGCGTGGATTCCT 556

QY 166 AlaleuLeuLeuThrIleProAspPheIlePheAlaAspValSerGlnGlyAspIleSer 185
DB 557 GCCCTCCGCTGACATATCCGACTTCTCTTGGCAACGTC-----AGT 601
QY 186 GlnGlyAspAspArgTyRLeuCysAspArgLeuTyRProAspSerLeuTrpMetValAl 205
DB 602 GAGGACATGACAGATATATCTGTACCGCTTACCCCAATGACTGTGGGTGCTGTC 661
QY 206 PheGlnPheGlnHisIleMetValGlyLeuLeuProGlyIleValIleLeuSerCys 225
DB 662 TTCAGGTTTCAGCATCATGCTGCGCTTTCCTGCTGGATTTGATCTCTCTCCGTC 721
QY 226 TyrCysIleIleIleSerLysLeuSerHisSerLysGlnHisArgLysAlaLeu 245
DB 722 TATTGCATATCATCTCCACACTGTGCACACTCCAAAGGCCACCAAGGCCAGCCCTC 781
QY 246 LysThrThrValIleLeuIleLeuAlaPhePheAlaCysTrpLeuProTyRTrpValGly 265
DB 782 AAGACACAGCATTCATCTCCTGCGCTTTCGCTGTGGCTGCTTACTACATTTGGC 841
QY 266 IleSerIleAspSerPheIleLeuLeuGlyValIleLysGln-GlyCysAspPheGluSe 285
DB 842 ATCAGCATGACCTCTTCATCTCTCTGGAATCATCAAGAGGGGTGTGAGTTGAGAA 901
QY 285 rIleValHisIleYrTrpIleSerIleThrGluAlaLeuAlaPhePheHisCysCys-Leu 305
DB 902 CACGCTGACAGAGTGATTTTCATCACCAGAGGCCCTTACCTTCTCAGCTTTGGCTGA 961
QY 305 snProlIleLeuTyRAla-PheLeuGlyAla-LysPheLysSerSerAlaGlnHisAlaLe 324
DB 962 ACCCATCTCTATGCTTCTTCCCTTGGAGCCCAATTTAAACCTTTCGCCAGACGACT 1021
QY 324 uAsnSerMet-SerArgGlySerSerLeu 333
DB 1022 CCACCTGTGAAACAAAGGTTCCAGCCTC 1050
QY 333
DB 1050
RESULT 2
LOCUS B1762229
DEFINITION B1762229 910 bp mRNA linear EST 25-SEP-2001
603049139F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5189552 5',
mRNA sequence.
ACCESSION B1762229
VERSION B1762229.1 GI:15753807
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 910)
NIH-MGC <http://mgc.nci.nih.gov/>.
NATIONAL INSTITUTES OF HEALTH, Mammalian Gene Collection (MGC)
Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-riemail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: LLM14/73 row: m column: 09
High quality sequence stop: 827.
Location/Qualifiers

FEATURES
source

1. 910
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5189552"
/clone_lib="NIH_MGC_116"
/lab_host="DH10B"
/note="Organ: pooled colon, kidney, stomach; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA

source anonymous pool of 3 colons, age 26 yo male, 49 yo female, 71 yo male colon; 46 yo male kidney, and pool of 2 stomachs, 62 yo male and 70 yo female. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 023. Note: this is a NIH-MGC Library."

BASE COUNT 210 a 260 c 208 g 232 t
ORIGIN

Alignment Scores:

Pred. No.: 2,59e-142 Length: 910
Score: 1238.50 Matches: 240
Percent Similarity: 92.20% Conservative: 20
Best Local Similarity: 85.11% Mismatches: 15
Query Match: 66.34% Indels: 7
DB: 13 Gaps: 1

9-367-052-2 (1-359) x B1762229 (1-910)

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QY 6 ValSerIleTyrThSerAspAsnTyrSerGluValAlGlySerGlyAspTyrAspSer 25
DB 83 ATCACTATATACACTTCAGATTAACACCCGAGAAATGGCTCAGGGGACTATGACTCC 142
QY 26 AsnLysGluProCysPheArgAspGluAsnValHisPheAsnArgIlePheLeuProthr 45
DB 143 ATGAAGGAAACCTGTTCCGTAAGAAATGCTAATTCATAAATAATCTCTGCCACC 202
QY 46 IleTyrPheIleIlePheLeuThrGlyIleValAlGlyAsnGlyLeuValIleLeuValMet 65
DB 203 ATCTACTCCATCATCTTCTTAACGTGCGCATTTGGGCAATGATGCTGCTACTGCTCATG 262
QY 66 GlyTyrGlnLysLysLeuArgSerMetThrAspLysTyrArgLeuHisLeuSerValAla 85
DB 263 GGTTCACGAGAAACTGAGAGCATGACGAGCAAGTACAGGCTGCACCTGCAGTGCC 322
QY 86 AspLeuLeuPheValIleThrLeuProPheThrPalaValAlaMetAlaAspTyrPyr 105
DB 323 GACCTCTCTTGTATACAGCTTCCTTGTGGAGTGTGATGCCGTGGCAACGTGTGTC 382
QY 106 PheGlyLysPheLeuCysLysAlaValHisIleIleTyrThValAsnLeuTyrSerSer 125
DB 383 TTGGGAAGCTTCATGACAGGCACTCATCATCTACACAGTCACTCCTACAGCACT 442
QY 126 ValLeuIleLeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThrAsn 145
DB 443 GTCCCTATCTGCTGCTCATGAGTGCACCTGACCTGCGCATGTCACGCCACCAAC 502
QY 146 SerGlnArgProArgLysLeuLeuAlaGluLysAlaValTyrValGlyValTrpIlePro 165
DB 503 AGCTGAGAGGCCAAGAGCTGTGGCTGAAAAGGTGCTATGTGGCTGTGGATCCT 562
QY 166 AlaLeuLeuLeuThrIleProAspPheIlePheAlaAspValSerGlnGlyAspIleSer 185
DB 563 GCCCTCGCTGCTGACTATCCGACCTTCATCTTGGCAACGTC-----AGT 607
QY 186 GlnGlyAspAspArgTyrIleCysAspArgLeuTyrProAspSerLeuTrpMetValVal 205
DB 608 GAGGAGCATGACAGATATATCTGTACCGCTTCCTCCCAAGACTTGTGGGTGTGG 667
QY 206 PheGlnPheGlnHisIleMetValGlyLeuIleLeuProGlyIleValIleLeuSerGys 225
DB 668 TACCGATTTCACACATCATGTTGGCTTATCTGCGCTGGGATTTGTCTCTGCTCC 727
QY 226 TyrCysIleIleIleSerLysLeuSerHisSerLysGlyHisGlnLysArgLysAlaLeu 245
DB 728 TATTCATATATCATCTCCAAAGCTGCACACCTCAAGGGCCACAGAGGCCAGGCCCTC 787
QY 246 LysThrThrValIleLeuIleLeuAlaPhePheAla-CysTrpLeuProTyrTyrValG 265
DB 788 CAGACCACAGTCATCTCTGCTTCTTGGCCCTGCTTGTGCTTACTACTTTGG 847

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QY 265 YlleSerIleAsp-SerPheIleLeuLenglyValIleLysGlnGlyCysAspPheGln 285
DB 848 GATCAGCATCGAATTCCTTTTCACTCTGGAATCATCAACCCAGGTGTACATTTGANA 907
QY 285 er 285
DB 908 AC 909

```

RESULT 3

B0718617

LOCUS

DEFINITION

AGENCOURT 8304537 lupski sympathetic_trunk Homo sapiens cDNA clone

IMAGE:6193609 5', mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 950)

NIH-MGC http://mgi.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgeapb@mail.nih.gov

Tissue Procurement: Dr. James R. Lupski

cDNA Library Preparation: Life Technologies, Inc.

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLNL3597 row: 1 column: 02

High quality sequence stop: 659.

Location/Qualifiers

1..950

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:6193609"

/clone_1ib="lupski_sympathetic_trunk"

/sex="male"

/tissue_type="sympathetic trunk"

/dev_stage="adult, 16 yr"

/lab_host="DH10B"

/note="Vector: PCMV-SPORT6 (Life Technologies); Site_1:

NotI; Site_2: SalI; cDNA made by oligo-dT priming.

Directionally cloned using the following adaptors:

5'-GACTAGTCTTACATGCGGAGCGGCGCT(15)-3'. Size selected >

1 kb for average insert length 1.9 kb. This is a primary

library, non-amplified. Library constructed by Life

Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor

College of Medicine); available through Life

Technologies."

BASE COUNT 223 a 270 c 217 g 238 t 2 others

ORIGIN

Alignment Scores:
Pred. No.: 5.11e-137 Length: 950
Score: 1196.00 Matches: 241
Percent Similarity: 88.51% Conservative: 21
Best Local Similarity: 81.42% Mismatches: 25
Query Match: 64.06% Indels: 9
DB: 14 Gaps: 2

US-09-367-052-2 (1-359) x B0718617 (1-950)

```

QY 6 ValSerIleTyrThSerAspAsnTyrSerGluValAlGlySerGlyAspTyrAspSer 25
DB 83 ATCACTATATACACTTCAGATTAACACCCGAGAAATGGCTCAGGGGACTATGACTCC 142

```


Db 544 GCCTCTCGTGCAGATATATCCCGCAATTTCATCTTGGCCAACTC-----AG 588
 QY 185 rGlAGlYAspAspArgrTyrlleCySaSPArGLeuTyTProAspSerleuTrpmetValVa 205
 Db 589 TGAGGCGAGATGACAGATATATCTGTGACCGCTTACCCCAATGACTTGTGGGTGTGT 648
 QY 205 lPhGGLPhedInIstIleMetValGlyLeuIleuProllylIleValIleuSerCy 225
 Db 649 GTTCACAGTTTCAGCACATCATGTGGCTTATCTCGCTGGTATGTGCATCCGTCTCTG 708
 QY 225 sTyfCyseIllelleSerlyLeuSerHisSerlysglyHisGlnlyArG-LysalAl 245
 Db 709 CTATTGCATTTCATCTCCAAAGCTGTCACTCCAAAGGCCACCAAGAAGCCAAAGGCC 768
 QY 245 euLystrH--ThValIleLeuIleLeuAlaPhePheAlaCysTrpLeuProTyTyrv 264
 Db 769 TCAAGAGCACCAAGTATCCCTCATCCGCGTTCTTTCGCGCTGTGGCTGTACTACAT 828
 264 alGlyIleSerIleAspSerPheIleLeuLeuGlyValIleLyGlnIlykysaspHe 283
 829 TGGGAATTCAGCATCACTTCCTCATCTCCCTCGGAATTCATCAACCAAGGTTGTAATT 887

RESULT	5
LOCUS	BM920800
DEFINITION	BM920800 1034 bp mRNA linear EST 12-MAR-2002 AGNCSCURF_6706081 NIH_MGC_115 Homo sapiens cDNA IMAGE:5752047 5', mRNA sequence.
ACCESSION	BM920800
VERSION	BM920800.1 GI:19371179
KEYWORDS	EST.
SOURCE	human. human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo. 1 (bases 1 to 1034) NIH-MGC http://mgc.ncl.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) unpublished (1999)
AUTHORS	Contact: Robert Strausberg, Ph.D.
JOURNAL	
COMMENT	

Email: cgabbs@email.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>
Plate: LLM12765 row: j column: 16
High quality sequence spot: 667.

FEATURES	Location/Qualifiers
source	1. .1034

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5752047"
/clone_1lb="NIH_MGC_115"
/lab_host="DH10B"
/notice="Organ: pooled brain, lung, testis; Vector:
pcmv-SpOEt6; Site:1: NotI; Site:2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dr primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH_MGC library."

```

Alignment Scores:	
Pred. No.:	7.47e-135
Score:	1179.00
Length:	1034
Matches:	243

Percent Similarity:	90.56%	Conservative:	16
Best Local Similarity:	84.97%	Mismatches:	11
Query Match:	63.15%	Indels:	16
DB:	14	Gaps:	3

US-09-367-052-2 (1-359) x BM920800 (1-1034)

6 ValSerIleTyrThrSerAspAsnTyrSerGluGluValGlySerGlyAspTyrAspSer 25

Db
86 ATCAGTATACACTTCAGTACTACACCGAGGAAATGGGCTCAAGGGACATTGACTCC 144

QY 26 ASNLysGLUProCysPheArgASPGLuASNValHisPheASNArgIlePheLeuProThr 45

Db 146 ATGAGGACCCCTGTTCCCGTGAAGAAATGCTAATTTCATTAATAATCTTCTGCCAC 20

QY 46 ILETyrPheIleIlePheLeuThrGlyIleValGlyAsnGlyLeuValIleLeuValMet 65

Db 206 ATCTACTCCATCATCTTCTTAACTGGCATTTGTGGCAATGGATTGGTCATCCCTGGTCATG 265

66 GlyTyrGlnLysLysLeuArgSerMetThrAspLysTyrArgLeuHisLeuSerValAla 85

Db 266 GGTTACCGAGAAGAACTGAGCAAGCAGGACGAGTACGAGGCTGCACCTGTCAGTGGCC 32

QY 86 ASPLLEuLPhEValIIEThLLeuPProHETrPalavaLaSPALeTaLaSPTryr 109
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Db 326 GACCTCCCTCTTGTTCATCAGCGTCCCTTCTGGCGAGTGATGCCCTGGCAACTGGTAC 38

QY 106 PhcglYlYsPhelcYlYsPhalaValHisILleIeTyrThrValasnlcYlYsSerSer 122

DB 386 TTGGGACCTTCCATAGCAGGCGAGTCCATGTACACTACACAGTCAACCTCTACAGCAGT 44

126 valbeulleleuuaipneileselbeuspargylleuuallevalahisatarnash 14

146 Sercg[narabroaraiustentona]ag[utusa]ava[thruva]ci[vva]trni]ebro 164

506 AGTCAGAGGCCAAGACTGTTGGCTGAAAGGTGGTCATATGTTGGCGTGGATCCT 561

166 AlaLeuLeuThrIleProAspPheIlePheAlaAspValSerGlnIleAspIleSer 18

Db
566 GCCCTCCGCTGACTATTCCGACTTATCTTTGCCAACGTC-----AGT 61

QY 186 GlnGlyAspAspArgTyrIleCysAspArgLeuTyrProAspSerLeuTrpMetValVal 20

Db 611 GAGCGAGATGACAGATATATCTGTGACCGCTTACCCCAATGACCTTGTGGGTGTG 67

QY 206 PheGlnPheGlnHisIleMetValGlyLeuIleLeuProGlyIleValIleLeuSerCys 22

Db 671 TTCAGTTTCAGCACATCATGTTGGCTTATCCTGCCCTGATTTGCATCCTGTCGCC 730

226 TyrCysIleIleIleSerLysLeuSerHisSerGlyGlyHis-GlnLysArgGlyAla-L 241

Db 731 TATTGCATTATCANCCTCCAAAGCTGTCACTCACTCCAAAGGCCACCCAGAGCGCAAGGCC 79

QY 245 euLysThrValIleLeuIleLeuAlaPhe-----PheAlaCysTrpLeuProT 26

Db 791 TCAGAGCACAGTCATCTCTATCTGCGCTTCTTCCGCCCTGTTTGGCTGC-----CCTA 84

QY 262 YRTYVal-GlyIleSerIleaspSer-PheIleIleuLeuGly-ValIleIleYs-GIinGly 28

Db 845 ACACATTTGGGATCAGCATGCACCTCTTCATCCTTCTGGAATCATCAAGCCAAGT 90

QY	281	Cysasp	282
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Db 905 TGTGAG 910

RESULT 6
B1761664

LOCUS	BT61664	827 bp	mRNA	linear	EST 25-SEP-20
DEFINITION	603046395F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5186878 5',				

ACCESSION	mRNA sequence, BI761664
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VERSION B1761664.1 GI:15753242
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 827)
 AUTHORS NIH-MGC <http://mgs.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
 Plate: L14M11466 row: m column: 23
 High quality sequence stop: 827.
 Location/Qualifiers
 1. 827
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:5166878"
 /clone_1lb="NIH_MGC_116"
 /lab_host="DH10B"
 /note="Organ: pooled colon, kidney, stomach; Vector:
 PCMV-SpORF; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
 source anonymous, pool of 3 colons, age 26 yo male, 49 yo
 female, 71 yo male colon; 46 yo male kidney, and pool of 2
 stomachs, 62 yo male and 70 yo female. Library is
 oligo-dT primed and directionally cloned (EcoRV site is
 destroyed upon cloning). Average insert size 1.4 kb,
 insert size range 1-3 kb. Library is normalized and
 enriched for full-length clones and was constructed by C.
 Gruber (Invitrogen). Research Genetics tracking code
 023. Note: this is a NIH-MGC library."
 BASE COUNT 190 a 232 c 194 g 210 t 1 others
 ORIGIN
 Alignment Scores:
 Pred. NO.: 6.04e-128 Length: 827
 Percent Similarity: 1122.00 Matches: 224
 Percent Similarity: 93.33% Conservative: 14
 Best Local Similarity: 87.84% Mismatches: 11
 Query Match: 60.10% Indels: 8
 Gaps: 13
 US-09-367-052-2 (1-359) x B1761664 (1-827)

Db 382 TTTGGAACTTCTCATGCAAGCGATGCTCATGATACAGCAACCTCTACAGAGT 441
 Oy 126 ValLeuIleLeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThrAsn 145
 Db 442 GTCCATCTCTGGCTTCATCAGCTGGACCGCTACCTGGCCATCTGCCACGCCACAC 501
 Oy 146 SerGlnArgProArgLysLeuAlaGlyAlaValTyrValGlyValTyrIlePro 165
 Db 502 AGTCAGAGCCCAAGAAAGCTGTGGCTGAAAGAGTGTATATGTNGCGCTGTGATCCT 561
 Oy 166 AlaLeuLeuLeuThrIleProAspPheIlePheAlaAspValSerGlnGlyAspIleSer 185
 Db 562 GCCCTCTGCTGACTATTCGCCGACTTCATCTTGGCCAACTC-----AGT 606
 Oy 186 GlnGlyAspAspArgTyrIleCysAspArgLeuTyrProAspSerLeuTyr-MetValVa 205
 Db 607 GAGGCAATACAGATATATCTGTGACCGCTTACCCCAATACCTGTGGTGGTGTCT 666
 Oy 205 lPheGlnPheGlnHisIleMetValGlyLeuIleLeuProGlyIleValIleLeuSerCy 225
 Db 667 GTTCAGATTTCAGACATCATGTTGGCTTATCTCCCTGATTTGTCTATCTCTGCTG 726
 Oy 225 sTyrCysIleIleIleSerLysLeuSerHisSerLysGlyHisGlnLysArgLysAla 245
 Db 727 CTATTCATATATCATCTCCAAAGCTGTACACATCCAAAGGCCACAGAGCGCAGGC-CT 784
 Oy 245 ulysThrThrValIleLeuIleLeuAlaPhePheAlaCysTyr 259
 Db 785 CAAAGACCAAGTCACTCTCATCTCGGCTTCTTGGCTGTGG 827
 RESULT 7
 BM051973
 LOCUS
 DEFINITION 60363887F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:5419890 5',
 mRNA sequence.
 ACCESSION BM051973
 VERSION BM051973.1 GI:16781240
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 913)
 AUTHORS NIH-MGC <http://mgs.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
 Plate: L14M1873 row: j column: 19
 High quality sequence stop: 723.
 Location/Qualifiers
 1. 913
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:5419890"
 /clone_1lb="NIH_MGC_8"
 /tissue_type="Burkitt lymphoma"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: lymph. Vector: pORF7; Site_1: XhoI; Site_2:
 EcoRI; cDNA made by oligo-dT priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGCAAGAG(g). Size-selected >500bp for average
 insert size 1.8kb. Library constructed by Ling Hong in
 the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit

BASE COUNT 217 a 254 c 215 g 227 t
ORIGIN

Alignment Scores:

Pred. No.: 6,64e-125 Length: 913
Score: 1098.00 Matches: 233
Percent Similarity: 88.38% Conservative: 18
Best Local Similarity: 82.04% Mismatches: 19
Query Match: 58.81% Indels: 14
DB: 13 Gaps: 2

US-09-367-052-2 (1-359) x BM051973 (1-913)

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*QY 6 ValSerIleTyrThrSerAspAsnTyrSerGluGluValAlaGlySerGlyAspTyrAspSer 25
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Db 82 ATCACTATATACACTTTCAGATTAACACCCGAGAAATGGGCTCAGGGGACTATGACTCC 141
QY 26 AsnLysGluProCysPheArgAspGluAsnValHisPheAsnArgIlePheLeuProThr 45
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Db 142 ATGAAGGAACCCGTGTTCCGTGAAGAAATGCTAATTCATAAATCTTCCTGCCAC 201
QY 46 IleTyrPheIleIlePheLeuThrGlyIleValGlyAsnGlyLeuValIleLeuValMet 65
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 202 ATCACTCCATCACTCTTCTTAACCTGGCAATGTGGCAATGATGTCATCCTGGTCATG 261
QY 66 GlyTyrGlnLysLysLeuArgSerMetThrAspLysTyrArgLeuHisLeuSerValAla 85
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 262 GGTTCACGAAGAAACTGAGAAAGCATGACGAGCAAGTACAGGCTGCACCTGTCAGTGGCC 321
QY 86 AspleuLeuPheValIleThrLeuProPheThrAlaValAspAlaMetAlaAspTyrPyr 105
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 322 GACCTCCTCTTGTGCATCAGCTTCCCTTGGGAGATTGATGCCGCAAACTGGTAC 381
QY 106 PheGlyLysPheLeuCysLysAlaValHisIleIleTyrThrValAsnLeuTyrSerSer 125
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 382 TTGGGAACCTTCATGACGAAGGCACTGCATCTACACAGTCAACCTCTACAGCAGT 441
QY 126 ValLeuIleLeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThrAsn 145
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Db 442 GTCCCATCCCTGGCTTATCATGAGTGGACCGCTACCTGGCCATGCTCCAGCCAC 501
QY 146 SerGlnArgProArgLysLeuLeuAlaGlyLysAlaValTyrValGlyValTyrPhePro 165
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 502 AGTCAGAGGCCAAGGAGCTGTGGCTGAAAAGGTGCTATGTGGGGTGTGATCCCT 561
QY 166 AlaLeuLeuLeuThrIleProAspPheIlePheAlaAspValSerGlnGlyAspIleSer 185
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 562 GCCCTCCCTGCTGACTATTCCGCACTTCATCTTTGCCAACGTC-----AGT 606
QY 186 GlnGlyAspAspArgTyrIleCysAspArgLeuTyrProAspSerLeuThrMet-ValVal 205
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 607 GAGGACAGATGACAGATATATCTGTGACCGTTCACCCCAATGACTTGGGGTGGATAGT 666
QY 205 IlePheGlnPheGlnHis-IleMetValGlyLeuLeuProGlyIleValIleLeuSer- 224
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 667 GTCCAGTTTTCAGCACCATCATGTTGGCTTATCTCCCTGCTATCCCATCTGCTCT 726
QY 225 CysTyrCysIleIleIleSerLysLeuSerHisSer-LysGlnHisGln-LysArgLysA 244
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 727 GACTTTCATATATCATCTCCAAAGCTGCACAACTCCAAAGGCCACCGAAGAGCCCAAGG 786
QY 244 IleuLeuLys---ThrThrValIleLeuIleLeu-AlaPhePheAlaCysTyr-LeuProTy 262
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 787 GCCTCAAAACACACGATCTCTCAATCTGAGCTTTCCTTGGCTTGGGCTATGCTTTA 846
QY 262 TTYr-ValGlyIleSerIleAspSerPheIleLeuLeuGlyValIleLysGlnGly 280
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 847 CTACACTGGGGATCGACATCGACTCCTTCATCTCCTGAGATCATCAAGCAGGGGT 902

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RESULT 8
B1756157
LOCUS

B1756157 875 bp mRNA linear EST 25-SEP-2001

DEFINITION 603030061F1 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:5200238 5',
mRNA sequence.
ACCESSION B1756157
VERSION B1756157.1 GI:15747735
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 875)
NIH-MGC <http://mgi.mcl.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Place: LNL1501 row: 3 column: 15
High quality sequence stop: 799.
Location/Qualifiers

FEATURES

source

1..875
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5200238"
/clone_11b="NIH_MGC_114"
/lab_host="DH10B"
/note="Organ: brain; Vector: pCMV-Sport6; Site: 1: NotI;
Site: 2: EcoRV (destroyed); RNA source anonymous pool of 6
male brains, age range 23-27 yo. Library is oligo-dT
primed and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.5 kb, insert size
range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 019. Note:
this is a NIH_MGC Library."
BASE COUNT 198 a 244 c 206 g 227 t
ORIGIN

Alignment Scores:

Pred. No.: 9.53e-125 Length: 875
Score: 1096.50 Matches: 229
Percent Similarity: 90.15% Conservative: 18
Best Local Similarity: 83.58% Mismatches: 17
Query Match: 58.73% Indels: 12
DB: 13 Gaps: 1

US-09-367-052-2 (1-359) x B1756157 (1-875)

```

QY 6 ValSerIleTyrThrSerAspAsnTyrSerGluGluValAlaGlySerGlyAspTyrAspSer 25
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Db 69 ATCACTATATACACTTTCAGATTAACACCCGAGAAATGGGCTCAGGGGACTATGACTCC 128
QY 26 AsnLysGluProCysPheArgAspGluAsnValHisPheAsnArgIlePheLeuProThr 45
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 129 ATGAAGGAACCCGTGTTCCGTGAAGAAATGCTAATTCATAAATCTTCCTGCCAC 188
QY 46 IleTyrPheIleIlePheLeuThrGlyIleValGlyAsnGlyLeuValIleLeuValMet 65
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 189 ATCTACTCATCATCTTCTTAACTGGCATGTGGGCAATGATGTCATCTGCTGTCATG 248
QY 66 GlyTyrGlnLysLysLeuArgSerMetThrAspLysTyrArgLeuHisLeuSerValAla 85
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 249 GGTTCACGAAGAAACTGAGAAAGCATGACGAGCAAGTACAGGCTGCACCTGTCAGTGGCC 308
QY 86 AspleuLeuPheValIleThrLeuProPheThrAlaValAspAlaMetAlaAspTyrPyr 105
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 309 GACCTCCTCTTGTGCATCAGCTTCCCTTGGGAGATTGATGCCGCAAACTGGTAC 368

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Oy		106	phecllylspshelucylsalavalahisrllellrthrvalanleutyrser	125
Db		369	tttgggaactctatgtcCAAGGCGTCCATGTCTACACAGTCACCTTTACAGAGT	428
Oy		126	ValleulleuleualpheilleSerLeuaspargyrLeualalleValahislatHsn	145
Db		429	GTCCTCATCTGGCCTTCATCAGTCTGGACCGCTACTGGCCATCGTCCAGCCACC	488
Oy		146	SerClnarprOarLysLeuleualagLuylsalavalTyrrValGllyalTrpIlepro	165
Db		489	AGTCAGAGGCCAAGAGAGCTTGTCGAAGAAGGTGCTATGTTGGCGTGCATCCCT	548
Oy		166	AlaleuleuleuthrlleproAsphellephenalaspyalSerGlnGlyAspIleSer	185
Db		549	GCCCTCGTGGCACTATTCCGACCTTCATCTTCCACAGTCT-----AGT	593
Oy		186	GlnGlyaspaspaqTyrrIleCyAsArg-LenTyrrProAsperLeutrPrmetVala	205
Db		594	GAGGCAGATGCACATATATCTGTGACCGCTTTCTACCCCACATACATTGTGGGTGGT	653
Db		205	LphgInPhedInHisIlemetValIGlyLeulelleuProGlyIleValIleleusercY	225
Oy		654	GTC-CAGTTTAGACATCATCAGTGTGGCCTTATCTGGCTGATGTGCATCTGCTCTG	712
Db		713	CTATAGCCTTTATCATCTCCAAAGCTGGTAACATCTCCAAAGGCCACAGAGCCAGGCG	772
Oy		225	sTYrcysile-IleIleserLysleuser-Hisser-LysGLyhIsGlnLysArGlySal	244
Db		244	aLeuLysThrThrvallleuleulleuAlaPhePhalaecystrrpeuprotyrrTyra	264
Oy		773	-CTAGGAAACAACATCATCTCATCTCGGTGCTTCTGCGGTGGCGTGTACTACAT	831
Db		264	I-GlyIleSerIleAspSerPheIleleuleu	274
Oy		832	TGGGAATAGATCGAATCTCTATCTCTCTG	863
RESULT 9				
LOCUS	B1754094	905 bp	mRNA	linear EST 25-SEP-2001
DEFINITION	603027651p1 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:5197836 5',			
ACCESSION	B1754094			
VERSION	B1754094.1	GI:15745672		
KEYWORDS	EST.			
SOURCE	human.			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
REMARKS	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
JOURNAL	NIH-MGC http://mgc.nci.nih.gov/.			
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC)			
	Unpublished (1999)			
	Contact: Robert Strausberg, Ph.D.			
	Email: cs9pbs@remail.nih.gov			
	Tissue Procurement: Life Technologies, Inc.			
	cDNA Library Preparation: Life Technologies, Inc.			
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)			
	DNA Sequencing by: Incyte Genomics, Inc.			
	Clone distribution: MGC clone distribution information can be			
	found through the I.M.A.G.E. Consortium/LNLN at:			
	http://image.lnl.nih.gov			
	Plate: LLM11495 row: f column: 13			
	High quality sequence stop: 807.			
FEATURES	Location/Qualifiers			

FEATURES

source

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/organism="Homo sapiens"
/db_xref="taxon:3606"
/clone_image="5197836"
/clone_lib="NIH_MGC_114"
/lab_host="DH10B"
/note="Organ: brain; Vector: pCMV-Sport6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27 yo. Library is oligo-dT

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primed and directionally cloned (BCoRV site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gubert (Invitrogen). Research Genetics tracking code 019. Note: this is a NIH-MGC Library."

Alignment Scores:	
Pred. No.:	2,37e-124
Score:	1093.50
Percent Similarity:	89.47%
Best Local Similarity:	83.51%
Query Match:	58.57%
DB:	13
	Gaps:
	3

US-09-367-052-2 (1-359) X B1754094 (1-905)

QY	6	valserlletryrthseraspasnryrserglugluvalglysercglysphyrraspsr	25
Db	76	atcattatataatcacttcagatnactacacccgaggaatggctcagggagactatgatctcc	135
QY	26	asnlysgsluprocyspheatrgaspculsanvalhisphenarngillepheleuprothr	45
Db	136	atgaaggaaccctgtttccgtgaagaaatgctaatttcaataaatcttctccgccac	195
QY	46	lletryrphellellepheleuthrglyilevalglyasnglyleuvalilleleuvalmet	65
Db	196	atctactccatcatcttcttactgactggcattgtggcgaatgagattggtctactcctggctcattg	255
QY	66	glytryrglnlyslyleuaurgserrmetrrasplystryargleuhislenuservala	85
Db	256	ggtrtccagaaamaactgagaaagcatgacggacaagatpaaagcctggacctgtcagaggcc	315
QY	86	aspleuleuphevalillethrleuprophe <tr>palaivalaspalamealaasprtryr</tr>	105
Db	316	gacctcctctttgtatcatcgccttcccttctggcagattgattgacctggcamaactgctac	375
QY	106	pheglyyspheelucyslysalaivalhisilletryrthrvalasuleutyrserser	125
Db	376	tttggagacttccrtatgcgaagcagctccatgcatctatcacagtcacaccttcacacagct	435
QY	126	valleulleleualaaphelleserleuasparqtyrleualaallevalhislaatrpraen	145
Db	436	gtcccatcctcctggcccttcacagctggaccccttaccctggcattccacggccaccac	495
QY	146	serglnatgproarglylsreuleuualagulylsalavaltryrvalsllyaltryrpilepro	165
Db	496	actcagagcccaagagactgtttggctgaaaagtgcttaigtttggcgttgatcctcct	555
QY	166	alaleulleulleuthrilleproaspheillephealaasvalserglnslaspileser	185
Db	556	gccctccctcgtcactatattcccgactcattctttgccacagctc-----act	600
QY	186	glnglyaspasparqtyrillecysasparqleutyrr-proaspsrserleutrmethyla	205
Db	601	gagcgagatgacacagatattatctctgcacccttcaccaccaaaagacttgggtggcgctg	660
QY	205	lphegin-phelinhisilemetvalglyleulleupro-glyllevalille-leuse	224
Db	661	gtytccaggtttgacgacatcatcattgtggccttaattcctggcgtgtaattgcatcctcctgtc	720
QY	224	rcyslyrr-cysllellelleleserlys-leuserhisserlys-glyhisglnlysa <tr>rgly</tr>	243
Db	721	ctgctatrttgcatattatcatctccaaagactgtcacatcccaagggggccaccagaaaggcag	780
QY	243	salaleulystrhrthrvalilleleulleleualaaphelalaasvalcys <tr>trpleudrotyrty</tr>	263
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QY	263	valglylleserlle-----aspserphelleulleuglyvalilleysglncl	280

Db 838 CATTGAGATCAGATTCGAGATTCCTTC-----CTGGAATATCAGCAGG 891
 QY 280 Y 280
 Db 892 T 892
 RESULT 10
 BM387369
 LOCUS
 DEFINITION BM387369 765 bp mRNA linear EST 17-JAN-2002
 UI-R-CNI-cj-g-19-0-UI-s1 UI-R-CNI Rattus norvegicus cDNA clone
 UI-R-CNI-cj-g-19-0-UI 3', mRNA sequence.
 ACCESSION BM387369
 VERSION BM387369.1 GI:18187422
 KEYWORDS EST.
 SOURCE Norway rat.
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 1 (bases 1 to 765)
 ENCE Ronaldo, M.F., Lennon, G. and Soares, M.B.
 Normalization and subtraction: two approaches to facilitate gene
 discovery
 Genome Res. 6 (9), 791-806 (1996)
 JOURNAL
 MEDLINE
 COMMENT
 Contact: Soares, MB
 Program for Rat Gene Discovery and Mapping
 University of Iowa
 451 Eckstein Medical Research Building Iowa City, IA 52242, USA
 Tel: 319 335 8250
 Fax: 319 335 9565
 Email: msoares@blue.weeg.uiowa.edu
 The sequence contained an oligo-dT track that was present in the
 oligonucleotide that was used to prime the synthesis of first
 strand cDNA and therefore this may represent a bonafide poly A
 tail. The sequence tag present in the cDNA between the NotI site
 and the oligo-dT track served to identify it as a clone from the
 normalized cervix library cDNA Library Preparation: M.B. Soares Lab
 Clone distribution: clones will be available through Research
 Genetics (www.resgen.com)
 Seq primer: M13 Forward
 PolA-Tes.
 FEATURES
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 Location/Qualifiers
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 /dev_stage="adult"
 /lab_host="DH10B (Life Technologies)"
 /note="Vector: pT73D-Pac (Pharmacia) with a modified
 polylinker. Site_1: Not I; Site_2: Eco RI; The UI-R-CNI
 library is a subtracted library derived from the following
 pool of seven normalized rat libraries: normalized rat
 seminal vesicles, normalized rat penis, normalized rat
 bladder, normalized rat cervix, normalized rat brown
 adipose, normalized rat fundus, and normalized rat
 salivary gland. It was constructed according to the
 procedure described by Ronaldo, Lennon & Soares (Genome
 Research genome 6: 791-806, 1996). For construction of
 the CNI library, plasmid DNA from the pool of normalized
 libraries was electroporated into competent bacteria for
 the production of single-stranded circular DNA. This was
 then used as a tracer in a subtractive hybridization with
 a driver (PCR amplified inserts from a plasmid DNA template
 preparation) comprising: a) a pool of about 34,000 clones
 from the Rat Unigene Set corresponding to plates R-5-AA-NN
 excluding plates R-5-MM and MN. This pool represented 40%
 of the final driver population. b) a pool of about 29,000
 clones from subtracted libraries CA0 and CA1 corresponding
 to plates R-CA0-AMV through R-CA0-AXS, R-CA0-AXZ through
 R-CA0-BAZ, R-CA0-BFE through R-CA0-BHY, R-CA0-BJS,

R-CA0-BKE, R-CA0-BKG-H, R-CA0-BKJ-K, R-CA0-BKP through
 R-CA0-BKS, R-CA0-BKU-V, R-CA0-BLY through R-CA0-BMA,
 R-CA0-BMC through R-CA0-BME, R-CA0-BNS, R-CA0-BOB through
 R-CA0-BOJ, R-CA0-BPA through R-CA0-BRG, R-CA1-BBA through
 R-CA1-BDA, R-CA1-BHJ through R-CA1-BJF, R-CA1-BJR,
 R-CA1-BJT through R-CA1-BKB, R-CA1-BKD, R-CA1-BKI,
 R-CA1-BKT, R-CA1-BLE, R-CA1-BLF through R-CA1-BLN,
 R-CA1-BLS, R-CA1-BLV, R-CA1-BNR, R-CA1-BNR, and
 R-CA1-BLE. The resulting pool represented 20% of the
 final driver population. c) a pool of about 15,000 clones
 from non-normalized libraries CS0s, CT0s, CW0s, CX0s
 and normalized libraries CS0, CT0, CU0, CW0, and CX0
 corresponding to plates R-CS0s-CBP through R-CS0s-CBO,
 R-CT0s-CAM through R-CT0s-CAX, R-CU0s-CBP through
 R-CU0s-CCA, R-CW0s-CCB through R-CW0s-CCM, R-CX0s-CCN
 through R-CX0s-CCX, R-CS0-BSD, R-CS0-BTD through R-CS0-BTV
 through R-CX0s-CCX, R-CT0-BTW through R-CT0-BUP, R-CT0-BVN,
 R-CS0-BWV, R-CT0-BWV through R-CT0-BUP, R-CT0-BVN,
 R-CU0-BUQ through R-CU0-BVU, R-CW0-BVU through R-CW0-BMP,
 R-CW0-BXN through R-CW0-BXO, R-CX0-BWQ through R-CX0-BXM.
 The resulting pool represented 5% of the final driver
 population. d) a pool of about 5,000 clones (1,000 from
 non-normalized eye library CV0 and 4,000 from normalized
 eye library CV1) corresponding to plates R-CV0-BRH through
 R-CV0-BRR, R-CV1-BRS through R-CV1-BSC, R-CV1-BSE through
 R-CV1-BTC, and R-CV1-BVO through R-CV1-BVU. This pool
 represented about 5% of the final driver population. e) A
 pool of about 10,000 clones from subtracted library BS2,
 BV0 and BVOP (7.9.5 kb cDNA library fraction from rat
 whole embryo), and BX0 (0.5.7kb cDNA library fraction from
 rat whole embryo) corresponding to plates R-BS2-BB8
 through R-BS2-BFB, R-BV0-ANR through R-BV0-ANR, R-BVOP-AOI
 through R-BVOP-AOX, and R-BX0-AOY through R-BX0-ASH. The
 resulting pool represented 5% of the final driver
 population. f) a pool of about 7,000 clones from the
 seven non-normalized libraries that make up the tracer
 including CY0, CZ0, DA0, DB0, DC0, DD0, and DE0
 corresponding to plates R-CY0-BXP through R-CY0-BXZ,
 R-CZ0-BYA through R-CZ0-BYL, R-CZ0-BXB-C, R-DA0-BXJ
 through R-DA0-BYP, R-DA0-BYD through R-DA0-BZH, R-DB0-BYQ
 through R-DB0-BZA, R-DC0-BZI through R-DC0-BZQ, R-DD0-BAY
 through R-DD0-CBA, R-DD0-BZR through R-DD0-CAL,
 R-DD0-CBB-C, and R-DE0-CAB through R-DE0-CAL. The
 resulting pool represented about 10% of the final driver
 population. g) a pool of about 2,000 clones from the pool
 of normalized libraries, CN0, that makes up the tracer.
 The corresponding plates are R-CN0-BMW through R-CN0-BLD,
 R-CN0-BLG, R-CN0-BLP through R-CN0-BLR, R-CN0-BLT,
 R-CN0-BLW-X, R-CN0-BMB, and R-CN0-BMF through R-CN0-BML.
 This pool represented 5% of the final driver population.
 h) a pool of the 28 most abundant clones in the CN0 pool
 corresponding to the following addresses: bkw-a-09-0-UI,
 bkw-b-09-0-UI, bkw-b-11-0-UI, bkw-b-10-0-UI, bkw-d-01-0-UI,
 bkw-d-06-0-UI, bkw-g-08-0-UI, bkw-h-12-0-UI,
 bky-a-05-0-UI, bkz-a-06-0-UI, bkz-a-11-0-UI, bkz-c-06-0-UI,
 bkz-c-09-0-UI, bkz-d-10-0-UI, bla-a-11-0-UI,
 bla-a-02-0-UI, bla-f-04-0-UI, bla-g-07-0-UI, bla-g-12-0-UI,
 blb-a-12-0-UI, blb-f-02-0-UI, blc-a-11-0-UI,
 blc-e-95-0-UI, bld-1-08-0-UI, bld-f-02-0-UI, blg-h-04-0-UI,
 blr-a-05-0-UI, blt-f-08-0-UI. This pool represented 5%
 of the final driver population. i) One abundant CN0 clone
 (corresponding to the address bkz-a-11-0-UI) was digested
 with NotI and Eco RI and the resulting insert was gel
 purified. This purified insert was added directly to the
 driver so that it represented 5% of the final driver
 population.
 TAG_LIB=UI-R-CNI
 TAG_TISSUE=cervix
 TAG_SEQ=GACCA"

BASE COUNT 157 a 211 c 194 g 202 t 1 others
 ORIGIN
 Alignment Scores:
 Pred. No.: 1.33e-123 Length: 765

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 QY 213 ValGlyLeuLeuLeuProGlyIleValIleLeuSerCysTyrCysIleIleIleSer 232
 Db 526 GTTGGCGCTATCCTGGCTGTATGTATCATCTCTCCGATTCATGATATATCATTCGCA 585
 QY 232 sLeuSerHisSerLeuGlyHisGlnLysArgLysAlaLeuLysThrVal--IleLeu 251
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 QY 252 IleLeuAlaPhePheAlaCysTrpLeuProTyrTyrValGlyIleSerIleAspSerPhe 271
 Db 646 ATCTGTGCTTCTTCCGCTTACGCTTACCTTACCTTGGATTCACATGATCATCTCTTC 704
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 Db 705 ATCTCTCGATCATCATCAAGCAGCGGTGTGAGTTGAGAAC 746
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 DEFINITION mRNA sequence.
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 VERSION BI917014.1 GI:16180966
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 SOURCE human.
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 746)
 NIH-MGC http://mgi.nci.nih.gov/
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabs-r@mail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: L14M1610 row: 0 column: 21
 High quality sequence stop: 744.
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 Site:2: EcoRV (destroyed); RNA source anonymous pool of 3
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 and male age 26 weeks. Library is oligo-dT primed and
 directionally cloned (EcoRV site is destroyed upon
 cloning). Average insert size 1.7 kb, insert size range
 0.7-3.5 kb. Library is normalized and enriched for
 full-length clones and was constructed by C. Gruber
 (Invitrogen). Research Genetics tracking code 017. Note:
 this is a NIH_MGC library."
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 Db 668 GTACAGATTTCACACACATCATGTGGCTTATCTGCGGTATGTGTCATCTGTCTG 727
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 REFERENCE 1 (bases 1 to 782)
 NIH-MGC http://mgi.nci.nih.gov/
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabs-r@mail.nih.gov
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.


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Oy 98 ValAspAlaMetAlaAspTrpTyrPheGlyLysPheLeuCysLysAlaValHisIleIle 117
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VERSION BIS97875.1 GI:15490814
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SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 742)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaabs-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraiki
Toshiyuki and Piero Carninci (RIKEN)

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FEATURES
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constructed by M. Brownstein (NHGRI, National
Institutes of Health). Note: this is a NIH-MGC Library."
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Pred. No.: 2,296-110 Length: 742
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Query Match: 52.46% Indels: 7
DB: 13 Gaps: 1

US-09-367-052-2 (1-359) x BIS97875 (1-742)
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Oy      186 GlnGlyAspAspArgTyrIleCysAspArgLeuTyrProAspSerLeuTyr-MetValIva 205
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Oy      205 IPhcGln-PhcGlnHisIleMetValGlyLeuIleLeuProGlyIleValIle 222
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